

B



PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification 6 : C12Q 1/68</p>	<p>A2</p>	<p>(11) International Publication Number: WO 98/20165 (43) International Publication Date: 14 May 1998 (14.05.98)</p>
<p>(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAH, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).</p>		<p>(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LJ	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

- 1 -

BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

-2-

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

-3-

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

- 4 -

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

- 5 -

DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

-6-

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

-7-

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

20 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

- 8 -

conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

- 9 -

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

-10-

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
10
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

-11-

sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

-12-

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

-13-

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

-14-

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

-15-

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

-16-

match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15 $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$

-17-

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

- The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.
- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

-18-

incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

-19-

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

-20-

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

-21-

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

-22-

D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

-23-

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

- 24 -

Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

-25-

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

-26-

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

-27-

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

-28-

100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

-29-

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

-30-

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

-31-

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	CT	---		---	TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACCTAAAACACATGCCAGTTGGGAAGGCTCT GAAAACCTCAGTGCATATAGGAACACTTGAGACTAATGAAAGAGAGAGITGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAGCTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGTCTTTC/TAAGTTAATGCTGTGCTCIGTCAG
WI-10744	61	GC	---		---	AAGCCATTGACGTAACTCAGAGGTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTGAATT AAATGAGGTAAAGTTTCAGGCACCTCA
WI-9975	126	CT	---		---	GGGCAAAATTACCAGCAAAAAGTCAAAITACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACA TTACAGTAACTATGCAATCTTTTGTATATAGTATATCTGCCCAATGCCCTAGAATA[C/T]AGTG GGTCCCTAATAGTATTAGTCCCTTTTCTCCTCTCTCTCACTCTGAAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATCAATTTGATTTCTACTGAA
WI-8010	247	GT	---		---	GCTAGGTTTGTCTGTTGGCTGCTTCACTAGACTTGAGATGACTTGAATTTACAGTAATCCCTATGT GATGTAACCTAGCTAGACCTTCCCTTCTCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTTCATCTGTATTAATTTCTTCCCATATTAATTTCAAGGGAGTGGACAGGT CCCTGGCTGAAAGAAATAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	GC	---		---	GCCTGGCTATCTTTTAACTTTAACTGTATCTTTGGTGTCTTCCATCCTAGGATTCGCCTTATAAT CTTTGTCTGTCTGA[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAITCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTGGACTCTATAACAACCTCCAACAGAA
WI-5222	52	GC	---		---	GCCGGCTATCTTTTAACTTTAACTGTATCTTTGGTGTCTTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGTCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAITCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTGGACTCTATAACAACCTCCAACAGAA
WI-8007	242	CA	---		---	TATGCACCTCCACAAAAGCGATATAATTTAAAGTTTTTTTTCATTAGAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTACTAACTATAGTCTCTTGGAAAGAACACCCAAACCAATACTT ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-9823	97	CT	---		---	TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTGTTTGTAG TCTATATTCACACATATGAGTGAAATTTCTGTTGGGCAATGGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACCTATCATAGTATCCATTTAAACAGACCAACAAATGTATAAGAAATCCCTTTGTTTAC ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGAATCACC

WI-9651b	105 A T ---	---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTAGTACAAATTTCTGCTCGTCTTCAATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCTCTG TCTTAAACCTGTAATGGTATATTAATCCCTGGGTGGTGAATGCTCTC
WI-9651	139 T C ---	---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCCTTCCT ACTTGCTCCTAGTACAAATTTCTGCTCGTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CTTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCTCTGT CTTAAACCTGTAATGGTATATTAATCCCTGGGTGGTGAATGCTCTC
WI-7676b	309 A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCCTTGCTGCTGGGACTTGGCCCTGCTATTTTITG TATTTATGCTTAACTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTTGGTGGCTGCTGGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCCCGTCTCCTGGAGGCGATATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCCTTGCTGCTGGGACTTGGCCCTGCTATTTTITG TATTTATGCTTAACTCTTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGGCTTCTTGGTGGCTGCTGGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCGATATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTGTGCTGGGTCTGTTCACTCACTTCTCTCTCCAAATGAAGGATATTTAAGCATCATT CATCTGGCCCTTTTGTGAGTTTGAATAATTTTGTGTGATGACTCTATGCACATGATAAATTTGTA TGTCTGCTCTTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACTTATAGATAATTTAATAATCTTT
WI-9986	42 T C ---	---	---	TTGGTGAACCTCAGAAATAGGGAAATAGACAAATTTGAAT/A.CJGTACCCAGGAAACAAGAG CCCTGCACTTGAATCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATAGGCCAAAGTGGAGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTGCATGGCTCTATCCCTCTGCCCTCTC/CJCCACTCTTTGGAGCAAGGAGATGC AGCTGATTGTGTAAACAGCTCATTGTACAGTGTCTGTATGAATAA
WI-7224	134 T C ---	---	---	ATAACCCCTTGTGATGATATCAACCACTCACTAATTTATCACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAATCCTAAACATCAAACTTTCATCCATAAAATGTGAGCATTT /CIATTAACCAATAAATCTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAATAAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTATCATGCTAG

WI-10826	132	A C ---	---	TCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACAGCCTCTATTTTAACTGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAAGCAAGAACCTGCAJ/C JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGTCAGCCAGGACCCCATGGCA GAAAGCCCGAGCCTCTCCATCCCCCAG
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAGAACCTTGTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T --	---	AAACACACAGAATCATCAAGCACJATJATCTGTGTTTGAGATAATGATAGTCTGAGTCACCTAIG TAAGAAGTAACTCTGAATAGTAGGATAGTATTATCAITTCCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAAITTTTCAITTCATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACTGCCATGGTAGGACTTTTGATCACTAGGAAATAAGAACACTTTGAATGGICTTGCC TTTCAATAAAGAGTGACATGATTGAACATGTGTTTGTAGATAAAGGGCATT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGAAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAITTCCTTCCAAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A ---	---	TTCAITTCCTTCCAAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCTTACCTGTAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACTTCTCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGGAATCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCTTACCTGTAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACTTCTCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT

WI-7330	207 C T ---			AGGATGGAAGGACACGGGCGAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTGTGGCATATAGGTTT GTGACACAGAAGTCACTTTGGTGGCTAAGTTTACTAAGGAAAAAATAACTGAAAGATTAAAAAG TGAGAG[C/J]TGAAGAAGAAAAATGATAATGCTTCCAACTGTAGCTGCACAG
WI-9443	211 G A ---			TTAAAAAGAGTTCAGGTTGGTGAAGCAGAAAAAGGATGTGATTACAATTTAAATGAATCAGTCACCTT GCACAAATTAATCCTCTTGGCATATACAAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCCATCAGCTACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCACATGCCCACTT
WI-7166	59 C T ---			TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/J]TGGAT CATCAACAAGATTTCTTGTGCAAAATATTTGACTATTTCTGATCTTTCATCTTGACTAAATCTGTG ATTTCAAGCAGCATCTTCTGTTTAACTTGTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAAAT TAATGCTTTTTTATACTAGGCTACCTGTGGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C ---			GCCTTCCCCAGGAAGCGGGTCTTGGCTTGGAACTTCCAGAGAGAGGGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGTCTTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAOCCTGGCCACAGT[C/J]TGGGGGAGCAG AGCAGCAGGTGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188 G T ---	C		GCCTTCCCCAGGAAGCGGGTCTTGGCTTGGAACTTCCAGAGAGAGGGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGTCTTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAOCCTGGCCACAGT[C/J]TGGGGGAGCA GAGCAGCAGGTGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275 A G ---			GTACTTTAGGCTGTGGAGGTGGCATTTAGTGTGACCTTGCACCAAGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTGGCCCTCTCACCCCTATATG GCCATAAACTGCCTAAGCACTCAGGCCCTCCCACTCATCAOCCCTTGACACAGAGAAAGCACTC TGGTTCTATCCCTTGTACATAGAGATTGTCATGGGCGCTCTGGCTG
WI-7685	46 T C ---			TCAGTTCTAGTCTCTGCGGCGCACAGAAACTCTTTTGGGCTGT[C/J]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGACAGGTCTTGGAGCTGAGCCTCTCACCTGACTCTTCCGAAAAATCTCT CTTCTCTGAGGCTGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCTCTCTGCGGACTC CTGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTTCTGTCTC
WI-563	87 G A ---			TGTACCAATTTGTTATTTAGAGGTTTAAACATGGCCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGAGGCGCTCCCCT[G/A]CCCTGATCAIGTCTACCTAACTGCTACTCTTAACAATACTACTCC TGTGTTAGGGGATCCTAAGCCAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTTGGATAACCCAGGGCACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCTTCT GTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCC(C/A)GAGGCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCT(A/G)TCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC(A/G)GCCACTAGCCCTGAACCTTGACACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGG(C/T)ACCTACTTAGAGAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAAGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGGACCTACTTAG(A/G)ACAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAAGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACCTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAATAATTTGGGCATTTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCACCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACCTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAATAATTTGGGCATTTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCACCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC(A/G)TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGAA GAGT(C/A)GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTTA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTGT

WI-10673	94 C G ---	---	---	TCCCTTTATGACCCCAAGAGATAATTTATTAAACACCAATTACGTAGCAGGCCATGGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGCTGGGCCCCCTACCTGCCCAATCAATCCTGCCAATAATCCTGTCTATTGTTCATCCTG GAGATTGAAGGGAGGTCAAGTTGTTGTCAATGATTTGTCAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCATGCCCTTGAGGAGCGGGCCACCCAGATGCTGAATCCCTATCCCATCTG[T/C]GTATGAG TCCCATTTGCCCTTGAATTAGCATTCGTCTCCCCCAAAAAAGAAATGTGTCTATGAAGCTTTCTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCCTCATACGCCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCAACCCAGCTGTTACCAAGCCCGGAGGTGCAGCCCTTCCTCCC TGTCTCTG[C/A/C]TCTGACTCTCTTTGAGGTCCCCTGTATGTCTACCTCTGACTTCTGTGTCCCTCTG TGTCTGCTCTCATCCTCTCTTACTGGGCTGGGGCTAGCCCCAA
WI-4767b	173 C A ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATGTTT CTTGCCTTGAGAAATCCTAGAAAGCACACAGGGATGACA[C/A]AAATCACTAAGGAAATTCCTACTAAGA CTCCTCTAACCCACAGAGATTTTAACTT
WI-4767	50 A G ---	---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CCTCAGGTCTGGGTATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATG TTTCTTGCCTTGAGAAATCCTAGAAAGCACACAGGGATGACACAAATCACTAAGGAAATTCCTACTAAGAC TCTCTAACCCACAGAGATTTTAACTT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGT ACTTTGCAGATGGAAGAGGTTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718a	42 A T ---	C	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAG TCAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7227d	99 G C ---	---	---	AGGGAATTGTTGCTCCTCGAGGAAGCCCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTATCTTTTCAGACAAGCTTTAGCAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTTGCTCCTCGAGGAAGCCCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTATCTTTTCAGACAAGCTTTAGCAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93 G T ---	---	---	AGGGAATTGTTGCTCCTCGAGGAAGCCCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTATCTTTTCAGACAAGCTTTAGCAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTTGCTCCTCGAGGAAGCCCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTATCTTTTCAGACAAGCTTTAGCAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCCAATGCCTCTCCACGATGTCAAGGACTCCTGCTGCTCCTCGAGGTGGGAGACAAGGAACCTCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGTGATCCTTCATCGAACAACCTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAATGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA/NC/ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAGGACTCCTGTCTCTCTGGAGGTGGGAGACAAAGAAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTTGACCTGCCCTGGACTCCTATGATGGCTGTGTTGATATAATCA GATCATGCCCAAGACGGGCTCTGATAATCGCTTTGGCATGATTGCAATGGAGGGCAATGGGTCC CTGAGGAGAAATCTGGAGGAGCTG/GGATGATGAAGGTGATGTTGGAGGGGAGCACAGTGT CTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTTGACCTGCCCTGGACTCCTATGATGGCTGTGTTGATATAATCA TCAGATCATGCCCAAGACGGGCTCTGATAATCGCTTTGGCATGATTGCAATGGAGGGCAATGTC GTCCCTGAGGAGAAATCTGGAGGAGCTGATGATGAAGGTGATGTTGGAGGGGAGCACAGTGT TCTGTGGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTACC AGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAGTTCCCTCTGTACAGAGACA AAACGGCTCTGTTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTACC ACCAAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAGTTCCCTCTGTACAGAG ACAAACGGCTCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTCTTCTTCTACC ACCAAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCCAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAGTTCCCTCTGTACAGAG ACAAACGGCTCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGACCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAACCTG CCAGGCAAGCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGACCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAACCTG CCAGGCAAGCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---	---	---	GAAGCAACCAGAAAGATCTTTATCCCATCTAGATTATGCTGGTTCTCCAGACTCCTACGATTAA AATTGATGATGTGAACAACATGATGAGGTACTTAGATCTCAGTGCTTGCAGAAAGAAAGTTCJC GCTACCAATTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-1795a	47 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGTTTCCTCCAGACTCCTACGA TTAAATTGATGATGTGAACAACATGATGAGGTACTTAGATCTCAGTGCTTGCAGAAAGAAAGTC GCTACCAATTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATT
WI-10616d	136 GA ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CIGATAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 GA ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CIGATAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 CT ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTGCCA CGTAGCCTCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 GC ---	---	---	CACACAATTTGCAACACTTCAAGTGAAGCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTACTCCACGTCTCCATACGTAGTCTGGTCTCCTATCACAATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 GA ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATATAATAAA AAACCCGTGAAGTCTGCTTGCATTTTCAAGATTCATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATTTAATTTCAAGTTCTCTCAAAAGGAATATGAAAT TGTTAAATGCAAAATCCAGCTGTAACTTTTGGACTTGTCTTTATTTCTT
WI-1126b	230 T C ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATATAATAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATTCATATATCCAGATTGTTTCCCAGCAAGAAAT TTATTTCTCAAGATATAAAAAATAAATTTAATTTCAAGTTCTCTCAAAAGGAATATGAAATTTGT AAAATGCAAAATCCAGCTGTAACTTTTCTTTGGACTTGTCTTTATTTCTT

WI-1126a	97	T C	---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTCCAGTATCACTGATATAATAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTC/CAATATATATCCAGATTTGTTTCCCGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAAATAATTTAAATTTTCAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACITTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/TAATAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAATATTTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/TAATAACA ATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAAT/CTATTTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCT/CTTGTCTACTAACA TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTTAAATATTTGGT ATGGGGTCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTTGGTTTGTCTTATGCTTATGCTCAGTCTTGGCTTCTCCCTTCTGCGTGGCCCTTTGTATTC CCCATACCTCTATGCTCTGCTCAGACCAATTTCTCTATCTGGAGCGCTTCTCTGTACTTTCTCTCG TTACCAACCTTCTTTTATCTTCAGGACACTCA/G/ATTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTTCTCCCTTCTCC
WI-10770a	49	G T	---			GCTTGGTTTGGTTTGTCTTATGCTCAGTCTTGGCTTCTCCCTTCTG/TCCTGGCCCTTTGTATTC TCACCCATACCTCTATGCTCTGCTCAGACCAATTTCTCTATCTGGAGCGCTTCTCTGTACTTTCTC CTGTTACCAACCTTCTTTTATCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTTCTCCCTTCTCC
WI-9667b	82	C T	---			GATGACAACCTTCTGCTGTGACCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA/C/TAAGCCACCTCCCGAGCGGCTTAGAAGCTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATCT
WI-9667a	68	G C	---			GATGACAACCTTCTGCTGTGACCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCTGTATCATG GCTTATCACTGGACACAGCCACCTCCCGAGCGGCTTAGAAGCTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATCT

WI-10400d	189 A G	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCACTTACTTGCATAATTATCAAGGCGTTAATGCATTATG
WI-10400c	166 A C	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCACTTACTTGCATAATTATCAAGGCGTTAATGCATTATG
WI-10400b	165 A G	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTCTAATTTT TCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGTAG TTTTTGGTTCACTTACTTGCATAATTATCAAGGCGTTAATGCATTATG
WI-10400a	46 T C	ACATTTTATTAGCAAAATCAGCAAAATAAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATAACGTAGTACCTATGTCTG G GCCATGT AGTTTGGTTCACTTACTTGCATAATTATCAAGGCGTTAATGCATTATG
WI-10809b	78 C T	AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTCACCAC C TTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATCTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCGGGTATGGACCAAAAGTCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T	AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGAG CCCCACCTCTACCACTTAGAAAGGGCATTTCAAGCACATTCATAGGCTTCATATCTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGGGTATGGACCAAAAGTCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C	CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGAAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACACAGCAIACAGTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGATGTTCTGAGTCC
WI-7038b	140 A C	CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAG AAGAA C GACTGTCAGGAAGGGTCGGAGTCTGTAAACACAGCAIACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGATGTTCTGAG

WI-7038a	31	G A ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGC[G]A[CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGGCA GACAAGAAGACTGTCAAGAAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCCTGCAITTTATGGTGTAGTTCTGA
WI-3429b	64	G T ---	---	ATACGTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTGCATGTCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	ATACGTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[CT]AG CCCTCAGCCCCCTCAGCTTGCATGTCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGACCT GTGAGCCCCATTCTCT[G]A[GTGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTCAGTTTCATCAT
WI-6786b	111	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGA CCGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTCAGTTTCATCAT
WI-6786a	106	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[AT]GGATAAAGAGTGAAGTGACGGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCTCTGGGTGCTCTATGTCAGTTTCATCAT
WI-6711b	226	G T ---	---	GGCTATTTGTAATGCTTGGTATTTGACTCCAAAATGTAATAAGTATGGGGAAGAATCCCTCACCT ACTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTACTGAAAT TTCATATACCTCCATTATTAATTAATCAATCATATTGCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTAACTCTCTAAA
WI-6711a	361	T C ---	---	GGCTATTTGTAATGCTTGGTATTTGACTCCAAAATGTAATAAGTATGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTACTCT GAATTCATATACCTCCATTATTAATTAATCAATCATATTGCAGAGAAAAGACACGGTGCCCAACTG GGTTGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTAACTCTCTAAA

WI-10613b	172 A C ---	---	---	ATTGTATGCCAAATCATAATACCTGCAATCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTTATTTGACGCCCCAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTCCACTCTATAATTTTAAGTCTCGGACTAGGAATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAATCATAATACCTGCAATCTAGAAACATACAGTGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTGACAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAGGCTCTTACCTCCACTCTATAATTTTAAGTCTCGGACTAGGAATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAACCTCAGGTAGTCTCCGAAGATCTGTGCTTCCAAAGTACTACCTTGAAGC ACATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAJ/ TJGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAACCTCAGGTAGTCTCCGAAGATCTGTGCTTCCAAAGTACTACCTTGAAGC ACATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAACCTCAGGTAGTCTCCGAAGATCTGTGCTTCCAAAGTACTACCTTGA AGCATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCCATTCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGCTGAGCCAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAACTCAATCAGCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCATTGACTTACGCAACTCAATCAGCAACC ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATGTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGCGTCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGTGTGACCCCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGGAGGGGGAATCCCTTGAACAGAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGAATTTTGTGAAGTTGTATTTCAAGACTCGAATTCATTTT

WI-7222b	255	GA	---	---	GCCTCCTCAACTGCTGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAAATTCCTTGAACAAGAAGAACTGGGATAGTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	GT	---	---	GCCTCCTCAACTGCTGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGAGGGGAAATTCCTTGAACAAGAAGAACTGGGATAGTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	CA	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTT(CA)TTATCTCCTCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237	GT	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTCAACGCCGCTTCCCTGGGCGTACAGAG(GT)AATCCTTGCCCTT
WI-8054b	148	TC	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGT(C)TTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131	CG	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C)GA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGGCGTACAGAGATCCTTGCCCTT
WI-10854b	152	GT	---	---	TTCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACACGAAAGACGATAGTTAACGCTCTGGTAAGTTAT ACGGTGTGCGAGGCAACAGTGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	CT	---	---	TTCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACAC(C)TGAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTGTTG

WI-9826b	127	G A	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTCTAGCCATGCTATTTTTGTG TGCTGATGGCTGTTGGTGTTCACGCAGTTGAGCCATTGTGACAGAGGCTGTAT[G/A]GCCTT CAAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGATTCTAGATATTTAAA GGCAGAGAATCAGAAAGTTTGAA
WI-9826	125	A T	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTCTAGCCATGCTATTTTTGTG TGCTGATGGCTGTTGGTGTTCACGCAGTTGAGCCATTGTGACAGAGGCTGTAT[G/A]GCCTT AAAGCCAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGATTCTAGATATTTAAA GCAGAGAATCAGAAAGTTTGAA
WI-15986	60	T G	TTGTTTGTGT GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTT/GTTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	AACTGCAAAAT AGGAAACCAG	CCACCTGGGG TOOC	TTCAAGTAACCTGCAAAATAGGAACCAAGAG[G/G]GGAGGCCAGGTGGGACAAATCATGGCTACCCC TCCCAACAGAACAGGGGGAGGAGGTGGGCCCTACACCCCTTAT
WI-8170b	259	G A	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAGTGCAATCCTATCAATCAGAA ATAAGGTAAAGGGCCCTCAATGAAATCTACGGAAAAACAACAAGA
WI-8170a	204	T A	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAATGAAATCTACGGAAAAACAACAAC
WI-8172	136	C G G A C A	CCTTATTAAA ATTGTTTCTT GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTCCAATCTCAGGTACATGTTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTATTTAAATGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTTATACATTTCTCTCACCGTTTACA
WI-8183	56	G A T G C	TGAATAAAA ACAATTTCTGT	TGTTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTG[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGTTAAAGACAAAAACCAAGCATGGGATTTTGC CGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAACACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCTG TTCTTAACAGCAGAGCCCGACCAACCTAGAGCGCCCTACCTAGCCCTCTTAAT

WI-8827	22 C T A C T A T G G	T C C C C T G G G A G	G C G A T T A G G A T	GGTGTCCCTGGGAGACTATGG(C)TAGTGAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTTCTTAGTTCCTTATCCACCCAGCTTCT
WI-8833	51 A T A T T C T C T G	T C T C C A T G C C	C C T C A C A C A T T	CTCCGGCCTCTAAAGCTCTCTGTAGACTGCTCTCCATGCCATTCTCTG(A)TJGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTTAGCCATGTGGTAAAGTTCAITTTTCAGTACATGGGTAAACCCAGGCCCTTTCCC(A)GJT TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTACTGTCTTCTTAGAGAG GCTACCAGGCTAAATTCACITTAGTTGGTTGTCTAATGTCTCATTTATCTCCTGAAGCTCGTG
WI-8850	21 A G C T T T G G C C T	G G G A C T T A A C	C A A A C A G C C A	GAGGGACTTAACCTTTGGCCT(A)GJCCTGCCCTGGCTTTGGCTCTGGCTTGTCTTTGGTTTCTT TCTCTTCTACTGGTCTTCTTCTTGTCTTTGCCAGCCACTAIGCTGT
WI-8853	79 C T A G G A T A	C C C G G C A T T G	A G T C T T C C T G A	ACTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATA(C)TATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGGTACTGGAATCACAGGCACAGACTGAGGAAGACAGTCTGGTGGAAACA(A)GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAA
WI-8865a	42 T C A	C A C A G A C T G A G G A A G A C A G T	G G T A A G T C C G A A G C A T G T T G	AGGGTACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA(T)CJGGTGGAAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCACCAACAGAAAT(A)CJCTCCCGTCTTTGAAATTTCCATTAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCACTCGACTGTGGACTGATATTTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA(G)CTTATGTCAAGTTAATAAAGATTCTAAGTGTCTCAGTC TCAACTTCTGTATTCTTGCCATGGTCCAGTAACAGTTCACAGGAGACCCACAAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGCTCTCAGTCACTCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAATGTGTATCAGTGCATATTCTATGGAAA ATTCAATCTCAAGTAAGCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA(A)GJTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAATGGTAATGTGTATCAGTGCATATTCTATGG AAAAATTCAATCTCAAGTAAGCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G C C A G C	G T G C A G G A A G	A A C G G C A G G A G G G G A	CTGCAGGTCTATGTGAGGAAGGCCAGC(A)GJTCCCTCTCTGCCGTGTGTCACCCACATCCACAGAGCA GCCCTAGTGCAGGTGAGCCACTGCCACCCACGCCACACGGGAACAGGCCCATGCTGC

WI-12108	40	C T A T A	TGAAAGGG TAAACTCAA	TGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAACTCAAAATATC/T]GAAATACTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29	G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCCTATGTA GG	CAGGCAACGTCACAAAGGTCACAGGCA/G]CGTACATACGGTCTGTATACCCCATATATTAC CCCTTCATGTCTTAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTCTTGGGTGAGGACACC
WI-12201	61	C T C T C A T G	CCACTGATCA OCTGCATG	CCGACCACATA OCTGGC	ATAGTCTTTTAGCCTTTTTCCTGGAGTGTATGTCCCAAGCCCACTGATCACTGCATGCT]GGCCA GGTATGGTCGGGGTGATGGACGTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTTATCTGTCAGGCAGCCAGCTCTGACTT/A]TCTCTCTGTCTTCTGTCTATCTCTCCCCACATACCA ACTTCTTACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC/A]G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTTA AGGATTAAGT	TCTTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTTGATGGTATATTGAGTTTCTAACCAGCTGAAAAATTCAAAATA CATGCCCTTTAAGGATTAAGTTTAA/A]G]CCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAATAATTATCTGTATACACATGTTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTAGTATTGTTCTGTCTATAATT]C]CCAAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAGCAATTTCAC/G]A]CTTCCAGAATACAAAGTACTTTAATACATATTTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTTCAGCATATGTTATTC/T] TGAACTAATTTACAAAGTGGAAACAGTTGGAAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGGC	ATACTGGTTTATCCATGTCAATGTAGTTTACAAAGGGAAAGGACAAAGTACCTTTGTATAGAAATAT ACAGACACAGCATCACACCA/C]T]AGGGCCCCACGGGAGGGTCCGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAGCAGGAGGAAAAATCCAATAAATTTTTTTTAA] A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAAATTGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C I G T G T G C C C C A	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATCTGCATCTCCTTTATGGATAAATCATGTGCCCCA/C]G]JAGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACAAATGTATCTGAAGAAGTATCTGTCTTGTC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTGTA GGACACTTACG	TGACACATGGTTCTGTTTCCAGAGGAGAGAGAGTCACTACATAAGCAGACACATAGTGGAA AGTCGCTAGTGTCTACGAGAGGTGAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCOCGCGCTGA GCAC	TTAGCCCATGCTGCTCATTGCAATCACCTGTGAACCTATGAAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTCGTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCCGCGGT GAITTCGATGCGTATAT
WI-11385	75	T C G	ACAGAGAGCT TTCATATCTT	GATTCATCTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCTGATGGTGGACACAGAGACTTTCATATCTTGTTTTAAAAAGTC TCTTCAGTCGAGGAAAAAGCTACAGATTAAAAAATATGACCATGACTAGATAAGAAATCAGC
WI-11388	88	C A A G T T C	TGTTTGAAT ACACGTAAC	TGCCTTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGGAGCTCATAAAAAATTAAAGAAATGAATGTTTG AAATTACACGTAACTAAGTTCGATATATATTTTAACTTGGATACAGGCAATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGTT CTTGAACCTTA	GTACATTCAAG TGTTTGTAAA	TTCTATCATCTCCATTAAATGGGAGGTTATGTGTTCTTGAACCTTAAATAAATACTCGCTTTTACA AAACACGTGATGATCTTCTTGTGAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTG AAATGGTGT	AGCTTATTTTC ATATCACCCA	AAAGAATAAGATGGCAATTTGTTCAAGTTAATTTGTTTGTAAATGGTGTGTTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A CAGC	TCCCACCAAC CAGC	TGOCAGGCGCT TATTTG	CTGTCAGCTTCTCCAACTAAACGTTCCAGTATGCTGGCAGCAGCTGCTGCTGTTCTTGGTG TATCCCATTAAGTGAATCCCAACCAACAGCAGCAGCAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGA	GTTTATTTGTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAGTCGCTTCAGTCCAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAATCTTCTATTATCTATTCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGCAGGAGGGAACAGTTGTCAATACTACCTTCTGTGG TCCCTGTAGACACATACCTTTCTTTGAAATGIAAAATGCA
WI-11276	41	A G A G C A G A C	GGCAGOCAGG AGCAGAC	TGTAAGGAGGA GCGGTG	AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGAGACAGCAGCAGCAGGCTCCTCAGTACACATT CCCAACCCCTGCTCGGTGCTCCCACTCAGGCTGGGCTGGGCGGAGGCGGTAGGCTCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACAA CTATTGCATAGGGAACAATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTAGTTCAATTACATGAGTACAAATCAATTAGAGCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAATTT GTACC	AATGGCTGGTTTTATTGAGAAGCTGTTGGTCATTTTGATGGAAAGACACATAC/TTGGTACAAAATT ACAGGTGGTTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAAGAGAACACACTTTGTGGGCTT[A] GTTCAACATGGACTGATAGGTCCTACCCAGATTCTAAGTGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGAGGAA AAAGAGGAA	TTGACAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCACCTTTTGAGATTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTTCAG AAA	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAATTTTTCAGAAAAAATAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACATATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCT AAA	TTTGAAAAGATGCTGAATTTTATCCCAAGTATAATTTTAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAAGGCAATTTCTTAAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATTT[C/T]CCAAGACCCGAGACTCCTCCAAAGTTCTCACTGTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTCTCACAGGTGTATTTGTTAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTCCTC
WI-11585	79 T C	TGGTTTGCAA AAACAAAA	CCATGCTTAC TGATACTTC	TTAGAAGGAAAGAAATAAAACACCGTAAATGGGAAATCAGTTTCAGAGGTAGGAAAGGAGCTGGTT TGCAAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTCGACGCTCACCATTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCCACTGGACTTGCCAACTTCACTGTGAAACTGCA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTG	AGGGTGGGAA ATGOC	CAAAATCAAAAATTGAGGAGGCAAGAAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCCACTGGACTTGCCAACTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGGTACAGGATAATATACTCAG ATATTTTAAAATAAA[T/C]TACTTAATAAAGAAATTAGCCATACCACATGTTCCATTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39 G A G	TCCACTGGAA CATGAAGGTA	GGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGACAGGATAATATACT CAGATAATTTTAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGGCTAC AAGAACAAATTGGCAATGA
WI-11627	23 T C	CCTTTCCTCC ATTGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTGCGCATGTCAAGTCCATCCATG
WI-11638	61 A G	GGACTTAAAA AGATCTGCTTA TCT	AGAACTTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATAATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCTCTTTTGGTA
WI-11537	119 C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAAATAAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTACAG TATACAATAATTAGAGAATAATTATGTTGCAATTGCTCATCTTACTCTGACCAAT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37 G C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACGCAACTG[C/A]AACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTCAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTGGGT
WI-11656	28 G A A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAATGTCTCTGAACAATCAGATTCCTCCAGCCTGGAT
WI-11680	55 T C	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C/TT]GCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47 T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCACCACATCTTGTTGTTTCAGAATCTTTCCACATCCGCC
WI-11702	69 C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACCAACAGC AG[C/T]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60 C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTCTTTGTACAATTTATTTGGCTG GAATTTGTTCTTTGGTGATTTGTCCTTGGCTGCT
WI-11709	105 T A	AGAAGCTTGC TTTCTGCTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAATTTAGAAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103 C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACAAACAGCCACACTCTAGACAGCCCTTCAC TCCAGTCCATTTCTGGCACTAGCCTCAGTCTTTCAC[C/A]CTCTCTCTCTCCACACTCTCTC

WI-11715b	123	C T	AGCTT	AGCTGGCTGC	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGGCTGGCTGCAGCTTCTJAGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A C A A A		GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGGTGTAAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGGCTGGCTGCAGCTTCAAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A		AACAATCCTT AAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTCTATACCTAACAAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAAATGAAACACAGATGCCCCAGACAGACCCCCACCACATGGCACACAC
WI-11728	16	C G	---		---	TTTTATTATCAAACT[C/G]CAATTCOCATTTCAAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTATCTCTTTCCACCCCTACACTTTCTCCCTACAACCCGGGTTCCAAA
WI-11758	61	A G T G C C T G		ATCTGTGGTTT TCGCTG	TGATTGGCCCT GTGGTCTA	TTTTTCTCTTTTATTAGTCGGCTATACTAACTAGAAAGGAGAATCTGTGGTTTCGCCTG[A/G]TAG ACCACAGGGCCAAATCACACAGCTTCTGTAGAGAACATGGAGAGTCCCAAGATCACCATCA
WI-11295	37	A G A A T A A A		GCCTCACAAA GTATTTTCTAA	AAAAGTGTCA TCTGTGAATC T	CCGGCCTCACAAAGTATTTCTAAATATAATTGCT[A/G]TAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C	---		---	AGCATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGATTAAGAAT ATTTATTGCCTCTTTTTCCTCCCT[C/G]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G G C A A G G G A A		GGCTCAGAGA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTATTAATGGCTCAGAGAGCAAGGAA[C/G]CACACAAAAATTTACAGTCTGA GTTTTGGCGGAGAGACCCCTCTCCACCTTTTTCATGCCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G A A C C T C T G		CCCAACTTACC	CGGTAGGGGAG GCTAAGC	TAATTCACCCAACTTACCAAACTCTG[A/G]GCTTAGCCTCGCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A		TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTCAGCTT ATAAAA	TTTTAATCCCAAAGCTTACAACCACTCTTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTTCTCTCTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T A A G T T T A A A		GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTCTCCCTTTTATAGTTTAAATGTGTTATAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[C/T]TGACAGCACAGTTCTTCAAGTTTGTCTATAGACAATCTGA AAATTGGGTTCTGAAC
WI-11906	52	A G A T C T G A A		TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT[A/G]TGAGGGAACCTG CAGAAATTAACTTTCAGTCTAATCTCAGAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTGTGTG GGTGGTCAAGAGTCTATTAGAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGGCCCAAGTTTGGCAGGCATGAAGAGTGGGCGAGTTCA/T/GIGTT TTATTAGTATAAAATGGCTTTACAGGAAGCATTTATGG CCCTAGTGAATACAAACCTTTGTCTGGAGAC/CAGCAGCTAGTCTAAGAAAACCTCTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAAGGGAA
WI-11946	31 C A	---	---	ACAAAAATCACAAGTACAACACTGCTTATTTTCTGCTTGAAGATCAGATCTCTGGTTATTTTAA/T/ GATCAACATTCCACACAGCTGAAGGAAATTAACCTGAACCT
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAAT/AJAATAAAATACTGTAAACATTTCTCATTTCTGTACGA ATACTTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGCACCTCCTCAATGCCGTG
WI-11027	90 T A A	---	TTTATT	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGGTTCAAAATAATTAAGGATCTTGACCTTT GTGTTATTTCTGTTTCAACTAAGGA/C/TAGACTTCAAGAGGCATAGCTTCCCTGTGAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-11049	95 C T	---	---	CAACATTTATCAACATGGTAGGGAAAAGTTCTCACTCTGCACATAAAAAGGACAGCCAGATATCA AC/C/TGTTACAGAAATGAAATAAGATGGAAAATTTTAAACAAATTG
WI-15488	69 C T A C	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCAATTTCTG TAAC	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA/GIGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C/C/TGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAGGGAA
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCA GTACCGTGGGGTCTTGATGACTTCCACGGTCACTGGGGATCCCAACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	AATCTTTATATTTCCAGCTTTGAGACAGTATTTTGAGGGCTGATTTTACCTCTAGCGGCAACCC AGAGCCAGCTATTAAAGCAGCCAGAAAAGCTACAGTAATTTGAATACATGACCAATTT/C/CTCTTTTAGC ACGTTCTTTGTTCTCTC
WI-12020	121 T C	---	---	

WI-11076b	142 G A ---				CATGGTCTGCCAGCTTACAGGAAGCATGGTGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGA ACTCTGAATTTATGGCAGTAGGCAWAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAATCTCACTCACTGTCAT
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG	GTATGTGAC	CATGTTCTGCCAGCTTACAGGAAGCATGGTGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGA ACTCTGAATTTATGGCAGTAGGCAAAAGGGGAGCAGGCA[T/C]GTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAATCTCACTCACTGTCAT
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA	AATTAGTATGG	GATATTCAAA	ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAAT[C/G]GTCCCATACTAAT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAAGTAACA AATTATGCTGAAATTAGGAAGGGAGCA[T/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGCAAGCAAGTACCATTCTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTT	TGATGATGCA		GATTTGTTTTATTCAATCTCGCTTTTCAATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50 G A TAGAAC	TGCTTTTAA	TATACTAAAA	ATCAAG	ACCTCTTCTGATGACACTGTACCTGTAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G/G]TCCAAGGGAAAGAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAAGAGATG GCTTCTTGTTAATCTGAGCA[G/C]ATTCAAGCAGCAATATTACTGAACACTTGCTATGTGCTG
WI-13951b	88 G C ---				G AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTTCTGTTAATTCTGGAGCAGATTCAAGCAGCAATATTACTGAACACTTGCTATGTGCTG
WI-13951a	39 C T CAAAA	GGAGTGAACA	TCCTCTGATC	TGGGGTCT	G GAGACCAAAAAGGGCTTGCCCAT[G/A]TATTCGGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGATCCCTTCTCTTGGGATCTGTGAATATAOCCA ACTGCTTGTCATGGC
WI-13264	25 G A TTGCCCAT	AAAAAGGCTC			TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[C/G]ATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAAAGTACTAACTTGTTCACTGTCATTTCCCTCACAAGGATTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA	AGCAAAAGGA	CATGAAAGGA		
WI-15843	62 C T CAG	ATCTTATAACC	CTCTGGCTCAG	ACTTGCTCT	AACCTCTTATTGTTAGTAGCCCCAGTGACTTTATGCATCTTATAOCAAAGAGCCTTCAAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGTCTCAGGGTCCACCAGGAACCAAGGCTTTGGCT

WI-13983	52 G A	TCTCTCCCACT CCCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACTCACTGACTTACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13950	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGGTTTATTTTATAGATTTTTTAACACAGCCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAGAATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCCCTTTGCCAACTATTCATTATTGACCACTCTTTTC CTCGTCAAGTGACCTGCCCATCATCAAGAAAGGCCCCGAAATATAGTGAGACTCA
WI-14284	55 C T	ATTTCAACAAATCCAGAACAGGTTCTCACACITTTGAGCCCTTTAGTGCACAAACAC[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C C C C A G A T	CCGCTGCTATT CC C C C A G A T	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAACGCCCTGTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTC C C A G A T [G/C] A G A T T T G T G G A A G G A G A C C A T G A C A G A T G A C A A A C G G
WI-13522	33 C T A C A A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAACTTGGAGAACCCTGACTTCAAAATATTATGAGAG AAATTACTCCAGGGAAATTTTGCAGAGAAGATAATA
WI-13529	42 T C T T A C C A	CACAAACATT TATTGAACAG	TCATATACACTT CTCACTCTCTT	AAATATGATTCCTATTCACAAACATTTATTTGAACAGTTACCACTTCCATTCAGAGGAGAGTGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGGTTATAGTCTAACAGGGGAAACACCTCTC A
WI-13859	84 G A	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]JACAAACAAGTATATATTCAGGAAAGGAGCTCCTAGAACTTGAGCA ACA
WI-13536	29 T C	TGAAAGGATACAGAAAAAACTCAGCGAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCACTTCCAGTTGTCTCTCCAGTCCCATGACATGAGTACACTTAATTTCTCAGCA
WI-13373	52 G A	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61 A G	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTCATTAGCTTGTCTTCAA[G/G]GAC AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAAGAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32 A G A G G	TAAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGGAG/GCATTGTTTTTCATTAGCTTGTCTTCAAAGAG AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAAGAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCAATGCAATTTATTTCTGGCAATAAATTAATATATGTCAGTTATAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAAATGTTTCTGAAATGTGCACACTAGATAATATGCAAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGATTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAGATTTTTTGGGACAATTACATGTTT AAAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGTCGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAACTCTAACTGCGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCAGCTTCAAAAATTTCTGCCTCCTAAAAACAATTTACAG CCAATTTTTCATATTGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAAAATGT CTGCCCATTTTGTGTAGCTTTTACAGTACAGATTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G TGTAATGCC	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGT GTAAATGCC[T/G]TTTACAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGTCAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAGAGAAAGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTCGAAGATGGGAAGGCAATTTTCATTTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATACT[T/G]GCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATCCAAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATTCGAAGATGGGAAGC[A/G]CATTTTTCATTTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-13763	59 T C GCAGTGAT	GGCTGGACACT	CCCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTCAACACTGGCTGGACACTGCAGTGAT[T/C]AGGG GCAGGTGTGGGCGAGGTGGGCCCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC[T/A]AGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTACCCAAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAGA GAGTCTCCCAAGAACCTC
WI-13789	62 G A AGGGAG	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCCTTGGGCA GTACTTTT	AATAACAAGTTTAAGTTCGAGTGCATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC G[A/T]GCACAAAAAGTACTGGCGCAAGGACAAATAATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	GTTCCTCCCACTAGTCCCGCAGAAAAAGGCATATTCAAGCTTGTGCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG CCCT	GTCTCACTTTCTGTCTAGGCTGTAATTTTCCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAAATTTACCCGAT GAAATCCAGTTATCTCT
WI-13600	26 G T	TAATGAGCC AAGCATCCAT	CTCACTTTAATGAGCCCAAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA ATATTAAT	GATAGGAAAGAAAGATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AATCTATTAAATATTGTCATGAGGTATGCACCT GCCC
WI-13650	76 A T	AAAGATTGAC AATATTTCACT TTTAAAC	GCATTAAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAGATTCAACAATTTTCAC TTTTAAAC[A/T]AAAAAATACTCTTCATATCCTAGCCTGATGACTTAAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGATATAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAAT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTA AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTTAAACTGTAAATCAATACATTTGCATTTCTTAAAA AAAGAAGACATTT[A/G]TTCCAGAGAAACCTGGGTATCATGCAGGAAAAGCAGAAAAAATTT
WI-13909c	93 A T	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTCAGAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAACATCAITCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAAATCAA GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAACATCAITCTGGACCTTGGACCTTGGAAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAGACTACCATTTATCAATTTTATATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[A/G]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGGCTTTTGTCTG[A/J]TTTGGGAAGACTACCAATTATTCAAATTTATT ATGTAATAGACTCATCGAGATAATGAACAATCTGCGAAAAGAGTGTGGGAATCACCTCATCTGTGC TGTAATCTGCTTACAGTCCCTTGGCAAAGACAGACATATGTTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGT[T/C]TTTAAATTATATGAACCTTTTGGTGAATTATGAAGTGTACCAAAAC C
WI-15747	88	T C A G T G T T	TGCTTCATTTT AAACTAATTT	CATAATTCACC AAAGTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGTGGATATACCTTGGCTTGCAQ[C/J]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752b	117	C T	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGTGGATATAC[T/C]TGGCTTGCAACCGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752a	106	T C A G T G T G A	CCTTCTCGTTA AGTGTCC	CCCTCCGTAAA AGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGTGGATATAC[T/C]TGGCTTGCAACCGACACCTTTTACG GAGGATTCGGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTAG[T/G]CGGTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAAACACGTAATGAACTTCATGACGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACTGAA[C/T]GCTGTGCTTATCTTTC CTGATCT
WI-13744	115	C T A A A C T G A A		GC	CCCTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/T]AACCAATTCATCCACCATTGTGTAATAATCTCATCTTCTGGGCTGGATACCAAAAAACAGAT
WI-14061	68	C T	TTACAGTTGGATTAACTACCACACTGAATATAC[TGAATTA]TAACCTTTCAACCCCTTTCATCCATTGAG C[A/C]AATTTAAACTCTTGCCAAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69	A C A T C A G C	ACCTTTTCATC CATTACG	TGACTTGGC AAGAGTTTAA ATT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACAGAAAGTACCACAGTATGCTTTATTITGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACTT[C/J]AGTTAGCAGCAAGCATCAGTCTTC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAAT	GGATTTTATTACATTTAAACTTGCAQ[G/J]TAGCAAAAAAATAACAAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAATTTCTCAATAGCATTTGGAAGGTTATTTCCATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACACAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACAACACAGTG
WI-15736a	27	G T C A C A	ATTTTATTAC ATTAACCTTG	GTCTTTGATA TGTTGGCTTAGT TTT	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[C/A]CAAAATG AACMGTGCTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785d	72	G A	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[C/A]CAAAATG AACMGTGCTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785c	56	A C	

WI-13785b	40	C G	---	TCAAAAGTGCACACTATAAAAGTCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTACACACACAGTG
WI-13785a	27	T C TGCT	AAACTGCAC ACTATAAAG	TGTTGTGACAG CTATGTGTAC T	TCAAAAGTGCACACTATAAAAGTCTTT[C/J]AAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTACACACACAGTG
WI-13793	88	C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAATAAAAATAGTTTTTACCCCCATTGATACACATAAAGGGATTT TACATTACAGCCTAGATATAG[C/G]AGTAACAATACTCTCTGCCATAAATCTATGACTTG
WI-13794	52	A G TTCTTTCTC	TTCTCACCCCT TTCTTTCTC	AGAAATGGGCTC TTAACCTTGTA	TAGTCTCTACAAATCCCTCAATCCATTTCTCTCTCACCCCTTTCTTTCTC[C/G]TACAAAGGTTAAGA GCCCATTTCTTCAAAACAACAAAACAACATAGAGCAAT
WI-15729	35	A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/G]GAGGCACCTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTTCCAAAGGAAGGTAAAGTCCCTGTTTGAGCCCCGGGGCTGCTCATTTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCTTTGCACAAAGTCTCCCAACTGGTTTGAGGTTTTTCCCTTCTGAGGTTTTTCCACCTATTCTTC[C/G] TAGACCTGGGAGAAAACACATGTGTAAGTGGCTCAGGACATGAGCAGGCCGTTTACAAAGAT GCTGGCTAAGGGCTTC
WI-14065	29	T C AAT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/G]AGATCCAGATTCAGCTTGTCTCATATAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATCTTGAAGCAGCAA
WI-13446	22	G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/G]CCTCTGATTTTGATTTCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C TGGGTGCC	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/A]GCCCGAG ACAGCAGGATAAGTTTTCACAAAATCTGACCAGGAGGTTAGAACCAAGGCATGGTTTCAGGATG
WI-15702d	107	T C ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACATACTAA[C/T]CJGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACATACTAA[C/T]CJGTGTAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T ...	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACATACTAATGGGTTCTTTGAACAAATAGTTT TGA

48	G C A A G	A A C A A A A T A A A G G C T T T C A A	O C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T A A T G G G T T C T T T G A A C A A A T A G T T T T G A
113	T C			T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T [G/C] G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
56	G C			T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
3	62	G A		T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A/C] C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
2	86	A G		C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G T C A A A T A A T A G G G A [G/T] T C T C T T T A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
3	95	A G		A G G C T G T T T T G A G G C C T G A G G A C C C C A A C A T G A C A A C G T A A G A C T G T A A C C A T G T A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C C A C C T C C C A A C G C C T T T A C T T T C A G C C T C T G C A
8	61	C T	G C A A G A A A G A A G T A A A T T A G G A A G A	A G A A C C G A G A A C T C A A A G A C C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G C A T G G A A G G A C T T T A G A T G G T C A C G
3	47	C T	A G A C T T G A G A G C T T A A A A C A A C A C T	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T T G C T T A A G G T C T T A C A A G G C C A A
5	31	A G	A G A A A A A A A T A A A A C T T C C T A T T T C T T	T G C A T T T A T T T T C A T G T A A G A A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
3	121	G C	T T G C T T A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T T C C A T T T T C T T T T G C T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
5	50	A G A T C	G G A G G G A G A T T T T A G A C T G A A G A A	T T G T T T T A T T T G G G G A A T G A A G G A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G T A T T T G A C G A C T A C A G C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G G G T T G C C A G A C A G

79	102	C T	CAOC	TCTATTAAACA GGGTATGTCA	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTGGTCTGCTCACTAATATCCAATCCTAGTATGATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C/T]TGTCACCTCAAACAGATGATACT TAAATAAAACAAAGCAGAAAA[C/A]CCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCGGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
02	22	C A	...	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAAGCGTCTGCGAGGGGCTGGGACCAGCTGC AGTGGGGCTCGGCACTGCTGCTCTCCAGGACTCTTCCCACCC
37	24	A G A	AACTGAAAG GTAATTCCTCC	AACTGAAAG GTAATTCCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTTATTTCTCCA[A/C]ACACGTTAGAACTTTAAAGCGGCAAAAGACTCACACCC ACACCTAGCGCGCAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACTGAAGGAT GGT
144	24	A C A				ATGTTTATGATCAATTCCAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAAAATAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAATGTGTTCAAATACTCAGCCAGAT CACCAAGCTCAGTCACTAC
24	92	A G	GACAAAGGCGCAGTTTCTGTAGTTCAGCAGGGCCAGAGAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGGACGACTA[C/T]GTGGCCATGCCATTCTCTGTAAGTGAATTAATGAACA
25	88	C T	CATAGATTTT	GGTTGACCTG CATAGATTTT	GGATGGCATG GOCAC	GTTATTTCTCACAGTTCTGGAGTTAGAGTCTGAGATGAGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGCTTCACAT[G/A]GCCCAAGAGAC AGAACAAAGCTCTCTGGT
36	120	G A	ATGCTTTCACA	GCTTCTCACC ATGCTTTCACA	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATCTGTAAACAAGACT GCATTAAATATTGTTTCTTAIGATTGTTTCAATG
138	23	C T	TGTTGGCAOCC GAAAAGCT	TGTTGGCAOCC GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTATTCTATAATTTTCAAACCTGGAAAGCAACCAAGATGTCCTTCAGTAGTATATCA GACAATC[G/A]AATATTACTTAGCCTAAAAAGAAATAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATAATTACT
351	74	G A	GACAATC	GACAATC	TAATATT	TTTTTAAGAGTGTCTTCACATCATTTATATTGATTGCACACAAACTTTTTTAACCTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC
b	59	C T	TTTTTAAGAGTGTCTTCACATCATTTATATTGATTGCACACAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC
a	26	T G A T	A	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG	TTTTTAAGAGTGTCTTCACATCATTTATATTGATTGCACACAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC

31	82	G A	---	---	TGAATCAATGGACAGTTTGCCTCTGTTTGTAGTGAACCCCTCACAAAGCACTCTGCATAGTCCGCTTTCTGTCTTTTAAAC[G/A]TGCCTGGTTCCCTCTGCCAAACITTTAGGATTGGCCCTCCTCAGGGCCCTTGTCCCTGA
34	24	A G	---	---	ATCACCAACCGTGTCTAAGAACAAAC[A/G]TCTTCATGTCCAACTCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCTCTGCATTGAACCTGGCTTCTCTGGAGGGAGCCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGAAGGGGTATATCTGGCTGGCCAGTTGGAAACACGGAG
34	99	T A	CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAAGTCTTGGCAAG
75	103	G A	GGCAC	CCCTTCTTTC TCTTCCCTC	CAGCTAAAGGATCAGTGCAGCTAAATACAGATAGAGAACCAACAAAGCCAGGCAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
79	96	G A	TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCACATAGTGGTGAGGCTGCACATTTTCTCTAGAAGGACATGAATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGGAGGAACAG
31	49	C G	ATTGT	CITATT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAAATTGTC[G/AAATAGTCAGAA
36	105	T A	---	---	AAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
37	31	C T	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATACAACTTCTACAACACATTCACAGAGCATATAACAAGAATTATTTACAGGCAGCTAATGTATTAAT[A/A]ACCATGAAAAAGAAAAACTTG
37	103	A C	AAATAAAAA	TG	ATCTAGATGTCAGCAAAATGGGCTGAGACTGTC[T/G]TGTCTGTAGATGACAGTGTGTATGTTCTAC
38	60	T A	G	TTACTTT	CTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATCACAGTC
33	47	C G	---	---	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCATTACAGAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACITTTAGGAGATGAAAAACACAAA
					TTAATAATTTAGCAAAAGTTATTGCAACAGGTTGAAATGCAGACACACTATTACAGGCTG[T/A]AAA
					GTAAACAATGAGTTTACACAATAAATAATTAACACATACTTATGGGATTTGTTGAATGA
					TTTTGTGTTAAGAACAGCATTTTGAATAAACCCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAAT
					TTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGC
					TTAGAAAACTGATAAAAGCAACACAACTTTTGGGAAGCACCATGGCAGCTCCTTTGTGCTA[C/T]
					GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
					ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAA
					AATCATCCCCCTTTTCATGATTGGAACAGITTTTCTGACCGCTCTGGAGCGTTGAAGGGTGACCAGC
15	22	G A	---	---	ACATTTGCACATGCAAAA

102	59	T C A G A A T T C	GATAACATAA AATGATCATG	GCCATCTCTC TTTGACTTTT	CCAAACATTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCAIT/CIGTTA AAAGTCAAAGAGGAGATGGCTAATGCATGGCTGGCT
3	101	A G A	CCCCTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAAGATAACACAT CTTCTTGCTCATCCACTTTGAACCTCAAGTCATCA/GJTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTTAACCA
59	73	T C GTGGG	GCCTTTGACTT	TCCACACTGC OCCC	TGAGTTACAACAAATGAGCAACAGTTAGAAAATTTGGTTTTATTCAAACTTCCTAGGTTGACTT GTGGGGT/CJGTACTCAAATGGGGGCAGTGTGGGACGGGAGGATTGCAACAGAGTTTCATACTG CAA
335	50	A T TAT	CTAGGAGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTACGGTGGTACTAGGAGGTTGAGGTGTAGATAT/ATCTTCCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATGCCCTTCTGTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCTCC
a	112	G A GGGAA	AAAGGCACAC	CTCAGCCTGOC TTGACC	TTCCATTTCATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAGGCACACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
340	18	T C ---		---	ACACAATATAATTCATTT/CJCGAGTGATTAAACCTATTTGTTGTTTAGAACCAAAACAAACTAC AAGAAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
308	52	T A CTAOCCTGT	ACCACCACA CTAOCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAAACACTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT/AJAAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACCTGAAGGGCCCCCATGTA
816	29	A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATT/ATJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
'c	71	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TTTAGGTGATTGATACAAATACGATCCATAA
'b	70	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/GTGTAGGTGATTGATACAAATACGATCCATAA
a	45	C T TTTAA	GCTATTAGGC AAACTGAACA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTTAAATGTC/ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
173	57	C T CAAAAA	GGATACAGCA GTAAGAATA	CCACCTCTAGA ATGTATGCTCT	CACCTAAATCATCTAGAACTGGGGATACAGCAGTAAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATTCTAGAGGTGGGAAAGAGGCAATAAATA

836	28 T C ---			TCCTTGGAGGGATAGAGGACAGAGTGTTCGTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGTCTAATTTGCCCCACCCTATAAAAAGCAGTGCCACCAGAGGCAG
856	60 A T A A	TGGTGACACG GAAAATACTT	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAACATAATATGATGGATGGTGACACGGAAAAATACTTTAAT[ATTTAA AGTTTGTAAAAAGTAGCAACAACAAATTTGAGTATATACTATATAAGTGATAGAGGATGATATGAAAAA GGCTATAAAAAGCTCCAAA
863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAAGGGCAATAATTTTTTGTCTGIG/AJAG TTAATAAAGTTAATAATCTTTTACCACAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTTAATTAACGTAAAAAGGAGGACATTTCCAAGGCTCTCTAAACA[TCGAGTGTCTGCGAGCCCCA TTCCGTTTGAGATGTGAATGTGTTAACCCAGGGTGG
733	98 G A A	CCAAATTGAC AGATAATTCTGC	GATGAGGTCAG GCCATTATT	ACGGAGTCGTCTGTGATGTTCTTGTCAAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAATT AGAAAAAATCCAAATTTGACAGATAATCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
lb	79 A C ---		---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAAAGTGGCCACTAAGGAAA ACTTCTCCAT[CA]AAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCGTGTCTGTCTT
a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATA[CA]AAGGTGCCACTAAGG AAACTTCTCCATAAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTCTGTCTT
907	48 G A G G A C T C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCTTGGCAGCAG ACATTTGTGAAGCTGCTGTGTGGCACACCCCAATCAATCAGTACTCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
911	52 G A C	CCAATACATT CAGTTCCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTCTGGT[G/A]AAGGTCCCTTTTC CTGGTTTGCAGACAGATACCTTGTGTATCCTCACATGGCAGAGAAAGAGGAAAGTAATCT
913	88 C A ---		---	CTGATGCTTTGACATCTGGGCAATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAAATTTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCACCT
914	66 G C A	CTGGACACAG TTTTCTTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGTCTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTTAGCA[G/ G]GAATTTATTGTCTCTGGGCTTGATGGCTTTTCACAGC
926	49 T C ---		---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAA[TC]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTTCAAGACAGTTTTTCAATAAAAAATTTTCTTAAATCAGGTCCA

33		ATGTTTAAACA	TGGAAGAAGATT	GCATCTTTATTACACAGAACTCATTTTATGTCTTAAATCATTTTAAATATATATATAAGCATGTT
39	C T	AAGGAT	CCAGCC	TAACACAAACATATCAAGGAT[C/T]GGGCTGGAACTCTTTTCCATTCTATAGAAAAGCACTAACCATC
30		GGAGGAGTCC	CACAACCAACC	CATTAAAGCAG
55	C T	CTCATGGAT	AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG
46	T C	---	---	GTTGGTTGTGGTATTGGGGAGCACGAGGGAGAGCAA
47	T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTGGCCCAAGACATAACA[C/T]CTCTAAATCATCTCTA
48	A G	---	---	GATCAGGGAGTCATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGGAAAGGATT
80	A G	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGACAC
32	C T	CACAAATTAAC	GGAGGCACTA	TAAGAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
56	T C G	AGGAACTG	CCAACTC	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGAG
52	A G	TTTCCCTACAC	GATGATCTTAC	CACCTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
58	A G	ATAAATTTAT	ATCACTTGTCA	GAATAAAGTCTTATTGCCGTCTCTCAGGGAACAGGAAACTGCTAACTTGTACG[C/T]TCCAACA
83	A G	CTCTTCTTTT	GA	ACTGATGAAGATCATCTCTGACCATTAGCGAACCTGTAAAGGCTGTGCTTCCCTCCAGCTGA
50	A G	TTGA	ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[C/G]TAATATACTG
58	A G	CAAAAAGCTA	ACAGGAATGTC	TTTCTGACATCTCTGTTATCAACTCTCTGAAATC
35	C T	TTTCCCTACAC	AGAAACAGT	GTGATTGATCTGTAATTTATGGGATTATTTATCAACTCTAAAATTCGAAGTGAATAATTTATCT
31	G T	ATAAATTTAT	AATGCAATCAT	CTTCTTTTCAAGGG[C/A/G]AAAAACCCCAATGAATGCATTTTCAGTTTCTCCAGGCCTTTGAACCTGC
76	C T	CTCTTCTTTT	TTGGGTTTT	AGCAGAAAAATTCAGGA
31	G T	CAAGGG	TCAAACTAAAT	TATTTTAAATTTGTTGATTGCTTCTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTTGGAGAG
35	C T	TCGTTCAAAG	CTTCCATTCTA	GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAGAAGATGCCCATCTCACACCTGGAG
31	G T	TCAGTGGTGT	AGC	ACGTCCATGAGCACCTCG
31	G T	TATTGGATTT	CACCTCTGACA	TAATTGATTCACTGGTGTATTGGATT[T/G/J]TTATGCTAAGTATTAATGTCAGAGGTGGAGAAT
31	G T	T	TAATACTTAGC	AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTGTGCACAGGAAGTTTGA
80	C T	TGCAATTAAT	ATAAA	GAGCTCACAAA
72	T A	---	GCTATGTGCTC	TGATTACATTTTTTAAATATCGCTTACCAGGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA
90	G A	GTCTAA	AGCTTTCCT	AATGAAGCTGCAG[C/T]AGGAAAGCTAGGACATAGCACCCCACTGATCGGAAAGAAACGTA
102	T A	---	---	AAATCTCTCTTTCACACACAGATGAACITTTAATAATTACAATGCACCTGAAAATGCCCTTCTTGA
90	G A	GTCTAA	CA	TTTCCCT[A/T]TCAGTTTAGGCCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAAGGCCCAAGTT
100	G A	GTCTAA	CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAACAGATGGATAGACAG
100	G A	GTCTAA	CA	AAAAAGACTCAGACTGTCTAAGT[A/G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

23	68	GA	CA	CAATACCTT CATGTACCTAT TTCCTACCTG	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACAAATACCTTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCACAAACAGAGGACTCACACCTGTGCTAGACAGCACC
33	91	A	T	AAGGACGAT TAGATCTAA TAAACA	GGCATGTCCA GTGTTTT	CATAAGTTGCATTATTACAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA/A/TJCAAAAAAACAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAACTAC
70	100	CA	T	CCTGCCCTTAT ATTGGAATTC T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAATTTAGGCAAGAGAAACAATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
2	38	T	A	CA TGAATGCTTC AAGTACAAAT	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAATCA/T/AJCTACAATACCATATACAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
2	40	A	C	TCTATTG TCTGGTATGC AATTGAAATA	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTGTCTATTTTATCTATTG/AJCTATTATAAGAAAAAGTGTGAGACCTT ATGGCTCTGCTTATGGCAATATGCAATATAATTTGTGTGTTTAAATTTAIGCAT
33	35	C	T	A AATGCACAAA ATCTGTCTCT	AA CAATTAACCTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAGTTTAAAGAGGACTATTTCTTTAAACAAGACAGTGTCTGACATTTATTTTCAAGT
33	88	T	A	TC CGCACTCTAA ATTAGAGATA	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTTATTATATTGGGAATTTGCAGTGATTAACATTTGTACAAAT GCACAAAATCTGTCTCTCTCT/TJ/TGTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTTGTCAT
7	58	T	C	GATTTT GATTTT	ATAAGATG ATAAGATG	CGGATATAATTATGTACCGCACTCTAAATAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACACAGTAGAACAGTTCACACCTGATAAATTCACAAGATG
2	17	GA	GCAGAACCAATTAAATG/AJATCTGCAAGTTTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATATAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
9	81	T	C	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTTTCCAGTATCATGTAC GCACATAAAAAA/T/CJGTGTGCTGTCTGTCTGTGAGTGAACCATTTGCTTAAAGATAAA
6	97	A	C	CCAGAGTGGC GCAGCAAGAT	AATTGTGTGCA TTTTGAAGAGA CTCCAAATAGC	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCAGAGTCGC/AJCTCTCTTCAAAATGCACACAAITTAAGACG
2	59	G	T	ATGT TAAGGT	CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTT[G/T]TACCT TACTATCTCTAGGCTATTTGGAGTGTCCCCCAG

3	62	T	G	TAAAT	TTTAACTTT TCTGGATGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAAAGTCTAATCGAGACATCACTGGGTATAAATTGA TATTTCTTTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAGGAAAAAGA ACAAATTTTCJTAAGAGACTTGGGGAGTGAAGGCAGAGCCTGGTCAGATGGACGAGGTCTGCAGA GG
7	74	C	T	AATTT	GACTTCAAAG GAAAAGAACA	TCACTCCCCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/CJ/CCTGCACGTGCACCTTTCATATACAGATCA TTTATTGGCTGCTCTGTAATACAATGTGGTGAACAC/G/ATCTTAATCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTATCAGTGG
5	95	C	A	GGACTCA	CCAATTTCTAG TGATAGTAGA	AAGGTGCAAGT GCAGG	AGAAATTTTTCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTTCAGAACTTCTCAAAATAC CTAGTTATTATACACATTCCTATCTGCTTGCAG/G/AGGAGGGATCTTGGTCGGCTTAAACA CCAGCTGGAGGTGGAATAATGCGGCAACCAAGAAAGAGGCGGACCTTTGATAAAGATGCT TGGCTTAT/CJ/GTGGCTGAAAAAGAGGCGGACCTTTGATAAAGATGCT
3	37	G	A	---	CATTOCCATCT GTCTTGCA	CCGACCAAGAT CCCTOC	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAATGCATAGGCACATCAGGATAAATACTG TTTGGTAAACTTGTTCAGTTAAATATGTAT/CJ/GTGTCCGTGCATGTATGATTAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACCAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCGACACCCACA
3	100	G	A	GGCTTA	GGCCTGCAAT GGCTTA	GGCCTTCTTT TCAGGCAC	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAATGCATAGGCACATCAGGATAAATACTG TTTGGTAAACTTGTTCAGTTT/CJ/AAATATGTATGTGTCCGTGCATGTATGATTAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACCAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCGACACCCACA
a	87	T	C	---	---	---	CACAACATTCAGAAGTTTCTGCATTGTGCTTCTCTGATGTCTAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTATAAGGTTTCTCCQ/CJ/AGTATGGATTCCTGATGATTAATA AGCCCCGAATTCCTGGCTAAAGGCTTCCACATTCACAGACATTTGAAGTTTCTCCAGTGGGAC TCTCTGGTTGCACAAGAATGGAACCTTGGCTGAATGCTTTCCACACT
1	32	G	A	ATGCAACAAG	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTAA TATTAGATAAAACCTTTGTTCCGATTGAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGTTTCAAAAGGACAGTT/AGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCCCTGTGAGGGATGCTGCCTTCAGGCCCTAAAG ACACTAGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
.	87	T	A	---	---	---	

91	A G G A T	G A C T G C T A A G G A T T T A A T T G T T A A A A	T G A A G T G T T A G A T G G C T A A G T A T T A A A A	A A G A G A C A A A T T A G C T C A G T C C A A C A T G A T T G G C A G T T G G C A T A T T C T A G T G A A G C A A G T G T T C T G A C T G C T A A G G A T T A A T T T G G A T A G A T T T A A T A C T A G C C A T C T A A C A C T T C A A G C A T A A C
105	T A G A A	C A C A T G G C A A T G A T A A T A A G A A A	T C T A T C C T C A G A G T G T A G T C T G C A	A A G T A G T G T C C T C A C A A A T A C A T T T C T C A A A C T C A A A C A T C A T G C T T G A A A T A T C A C T G A A C T T G T C A C C A A A G A A G T C A C A T G G C A A T G A T A A T A A A G A A T A A T G C A G A C T A C A C T C T G A G G A T A G A G C T C T A A A G A G T A A A A C A A T G G A A T T T G G A A A A A T A G G A G T A A A
164	C T ---	---	---	C A T A T G C T G C T T A T T C T G T A A G G A T A C A C T G A A A C G T T A G A T G A T A A T A G C T A A T A G C T A A T A G A C A A T G T A G A A A T G A G G C A T C A G C T T C T A A C C A C T C C T A C A A G A A T G T T A G T A T G T A T T G T C A T T A C A T G T T T A C T T T T G A T A T T G T C T C A T T A T A C T A T G T C T A T A T A A T A A T G T A G A A T A C A G T A A G T A G G T G A T C C T G C A T T C A G G T A A G C G G T A G G T G G A A T C C A G A T T C C T C T T G A G G A A A A
131	C T ---	---	---	C G G G T T A A G A A A T A C C T T T A A T T A G G T A A A T A A A G C T C A A G G A G G T G G G G C T G T C A T C T G T G G T G T C A G T C C T T C T G G C C C C T G G C T G C A G T G T C G C T C C A G G G C C T T G A C A A G C A G C T A T T C A A G C T G G C C C A C C A T G G C C C T A G G G T C G T C A A A G T C C A G A G C C A G C A T C A T G G C G T T C G T A T A T C T G A T C C A C
175	G A ---	---	---	A T A G C T T T A T T T G T C A A C G A A G G C T A C A C G G G A T C A C T T C T G G T T T G T T T A T G C T T T T T T T T T C T A G A A G G T A T C A C A T C T G C A T T A T T A C A G C C T T G T G G T A T T A C A C A G T C A A G A T A C A G T G T T A G A A C A C A A A A G T T G A G A A A A A A A C T T C T C A A A A T T G A G T T C C A G A C T T C A G G A A A T G A T T T C C A C A T G G T A A G C C A G A G T C C A G T T G G T C A T C C A G A A G C A G C T T G
86	C T T A A	G C A T T T A T T C A G G G A A A C T T A A	C T G T T T T T G G A G A A G A C A A A G A A	C T T G A T T T A A T C A G G G C T T G G G T C A T A G G G G A T T A G T C A C T G T C A C A G T C A T A A T A A T G C A T T T A T T C A G G G A A A C T T T A A T C T T T C T C T C C A A A A C A G C T G C T G G A A C A C C T C A A A T T A A G G G A T G T T C A T C T A A A C A C C T T T A C T G A A A C T T G A T T C C T T G G C C A G A G G A A G G C T T T A C T G T A G C A G A G G A C T T A A T G C A A T G C C T A T T C G G G C A A T A A A T G A A T A C T T G A T G C A T T C A T A C A G G C A A G A A T C C C A G C A T C C A G A G A A G C T G T G T G C G A G T G C A A A G C C A T G G C T G C A G A C A T C A G G G A A G C T G G T G C A G T T C T A G T C T G C C T C C T C G A T T T C C C T G C C A G C A G T C T C C T C T C T C A T T C T C T G G C C
96	G A C T C T G T C T G C	C C C A G A G A A G C T C T G T C T G C	C A G C C A T G G C T T T G C A G	T C T G A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T C A A G C C A G C G T G T C A T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A A C T G G A T A A A G A G T T G C T G A T A G T A G T G C T G T G G T T C T T C C C T T T A C A T T C T T T G G G G A
b 193	C T ---	---	---	A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T C A A G C C C A G C G T G T C A T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A A C T G G A T A A A G A G T T G C T G A T A G T G A T G C A G T T G C A G T T G C T T C C C T T T A C A T T C T T T G G G G A
187	T C ---	---	---	A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T C A A G C C C A G C G T G T C A T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A A C T G G A T A A A G A G T T G C T G A T A G T G A T G C A G T T G C A G T T G C T T C C C T T T A C A T T C T T T G G G G A

		GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAGAGTATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[TA]GCAACTGACAGTTTGAAG GACACCAAGACAAATAGGGCT
b	112	T A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[AT]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAAATAGGGCT
a	73	A T ---	---	CTAATATAATCCTGGGCACATGGATCCAAAGAGAGATTTTCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[GT]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
	165	G T GCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGGACGTCCTGGTAGTTCTCTCTTTTACACAACTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACGAAACAGCTAAAACTCTGAGAGAAAAAC[CG]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
b	68	C T ---	---	ATTGTAATTAATAATTTACATGGGCCTATTATTAAAGGACATTGTAATGTTCCACTTTGTTTAA [CT]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGCGG
la	42	G C ---	---	ATTGTAATTAATAATTTACATGGGCCTATTATTAAAGGACATT[CG]TGTAAATGTTCCACTTTGTTT AAACAATTTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGCGG AACCAAAACAACTAAGAAATGGGAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[TC]AGCAATGGATGCTGTGTGAGAACATACTGCCAATAAACTTTAAAGAAAAAGGA ACTCAATGAAGTTACTGTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCCAAAAC
p	75	T C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAAAATCAATCAAACTCCAGCTGTTTCTGCTTT TTACTTAGCAAAAGGAAACCTTAGTGAATGCTACTTGACAAGAAAGATCATTTTCTCAAGCACAI T[CG]ACCCAACTTGAAGGTGATTGAACCCCAAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTTGGCCAAAGCTATCTGGTTATATTGATGTTGGCAAT
i	134	T C ---	---	TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAACTACCAAAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[CT]GGCTAATACACTGCAATATTTA TGTTTAGCAAAATTATAGCTGTCTGTGTATACCAGAGAGCGGTATCTGG
jb	106	C T AGCCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

10a	28	T C A G A G	A A A C C C A C C A T T A T T A A G G	G C T G T G T T G G T A G T T T T C C T	T G C T A A A C A C C A C C A T T A T T A A G G A G A G T C J A C T A G G A A A A A C T A C C A A C A C A G C A T G T G A A A C A G T T G G C A C G G T G T A A A G G G C A C A G A C T C T G G A G C C A G C C G G C T A A T A C A C T G C A A T A T T T A T G T T A G C A A T T A T A C T G G T C T G T G T A T A C C A G A A G A G C G G T A T C T G G
10	53	A G A A C A T C A C A	C A A C C C C A A A A C A T C A C A	G C T T T T G G A G T G T A T A A T A G T A	G A T G T T A A T G A C A C A G A T C T C C C A A A G T A A T C C A A A C C C A A A C A C A C A C A J A G J A A T T A T T C A T A C T A T T A T A C A C T C C A A A G C A A A T A C T T C A A C T G C A A T C C
36	151	A G A	G C A T T C T T C C A A A A C A A A G A	C C T T G T A A G T G A C T A T T C C A A T	A T T C T G A G G C A A A G G T T C A G A A A T C A G C T A G C A C T A T A T C T T G A C C A A T G G G T G A G T C A G C C T C A T C A C A G A G A T T T T T T T A A T T A G A T G A A T T T C A C A T T T A A A A C A T G G T A A C T C C A A G C A T T C T T C C A A A A C A A A G A A T J A G J A C A T T G G A A T A G T C A C T T A C A A G G A C
31	32	C A G	G A T C T A A C A G C T G C A G A A T G	A A A A G C T G G G A A G G A A G A G	C C T G A G A G C A G A T C T A A C A G C T G C A G A A T G G J C A J C T T C T C C T T C C A G C T T T T G T G A C A A A A C A A T T C T C T A A G C C A T C A G A A A G C A C T G A G T G C A A A A T G G T T G T T C A G G T A C A A G G T C T C
14	225	T C		---	T A A A T A C T G C C A A C T A G C A T T A C G T C C A C T C T T G C A T C A T T A A A A C A A A G G G T A T T T C C T C C T T G G T A T T T C A A A T G A T G C A T T A T A C A A T A A A C G A A G T T A G A A C T T A A A T G C A C C C T G A T T A A T A T G T A A A C T G G T A A T T T G T T T A A A A A G C A T A A T A A T T G G T T C C T T C T T C A T A A A A T G G A A T T T A A A T A T T C T C T G A T A G C T T G A G G T J C J A T C A T T A G T A G T A G C A A A G T G T G
24	112	A G		---	C G G T T T G C T A C A C T T A A T G G G T T T T T T A A G G A T T T T T T C A G G T C T T G T C A G C A A C A T C A A A C A A A G G T A C T G A G T A C C A C A G G G T A C A G A G T G C T G C C A J A G J C A C C T T A G A A A A A T T A C A T G A C A C G A G A A A A T G C G C T C T T G C T C T T G A A G A G C T T A C A G C T A G G G A T T T G A C A A C T C A C A G T C T T A G G A A C T G G G C A A A G T A A G G C A A T T C T C A T C C C C T A G A G C T A T T G T G
39	139	T C A A T T C	G A A A A A T G A G A T G C A G T T A A	T C A C T T T G T G G C T T T T A A T T A T	G T A C A A A A A A G C T G A A G A G C C A C A C A T G G A A G T G T C A A G A A A A C A T T C T G A T A G G T A C G G A C A A A A G A G C T C C T T C A A T C A A A G G A G T T A C A T A T T A G T T C T C A C C A T G C T A G A A A A A T G A G A T G C A G T T A A A A T T C T J C J A G A A T A A T T A A A G C C A C A A A G A A A C T G T T G T T C T G G G C C C T A T G T T G T A G A T T C T C T
11	216	T C		---	T C C C C A G C T C A T A T T T A T T T G G C A C A G A G T G G G C A C T C A A A T A T C T G A T G A A C T T G A A C T G A A A A G A G G T C C C T T A A C A A G A T A T C A T C T C C G A A G A G A A A G T C C C A C C A T A T A A A T G A T G A T C A A G T C C A G A A A A C T T T G C C T T C C C A A G G A A T G T T T C A A T T G G T T C A A A G C A C A C T G G T T C C C A C T T T A C C A C T T J C J A T G A C A T T G G A C A A T A G T A C T A C T C T T T T C T A C
13	112	G C		---	G C C A G T C T C T A G T A A G T C T A G G G A C A T G A C C A G A C C A A G A A G C C C T G T T C T A T A T A G A G A C A A A C A G G T G G C C A T A C T T G G T G A G G G A T A C C G C T A T T C C C A G A T J C J A G A T T T G T G G A A G G A G A C C A T G A C A G A T G A C A A C G G A A C A G T T T C T C A A A A C A G A G G T A T G A
57	74	C T		---	A A A G C T T T A A A A A A A A G T G G T G C T A T C T T T A G A A A C A C T T T C A G C A A G A T C A A G T A G C C C A G C T A C A G C C T J C J G G T G C A T C T T A A C C C C T C C C T T T

37	G T	---	---	TGCTCTTTTATTACAGTTTCACAACACACGCCGTG[G/TTGGCACAGTCTACCAAGTGCCCGCAGCGCCACGCTTGGCGGGAAGGTCATCTGTCGTCTCTATGGACTGATTGAATTTGGATGGCCAGCTCCAGAAATGTTCCACGTGGGGCACTCTGTGGGCAGAGGCTGAGCCCTTGCCACACTGGCAOCCAAGAGGTTGCACGATGCAGCTTGCAGTGGGTCCAAGCCGGGTGCTGTG
7	121	T G	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTATCATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAATAAAGT[G/ATAAATCTTTGATTAATAAATGTTTATAAATGTTTATGAAGCTCAATACATTATCTTTTAAAAAAGTAAAAATTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
114	G C	GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATG[G/CACACCCACACCTGGTTAACTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAAC
51	C G	---	---	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]ACAGTAGCCTCAACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCCACACCTGGTTAATTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAACCAACTAA
12	71	C T	AGCTTTT	C ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTTTTTCCTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGTTTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTAAATTGAGGGAATAGGCCAATTT
188	36	C A	CTCAGTACAA GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGGTACACTTTGATAAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACATCTTTATGGAAACTGTTTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGTAAA
a	108	G A	CTTT	TGCTATTCATGACAGACACGTCGAGACAAATATCTTATTTTACAGATGGAATAGACCCAGACATTATTTCAGTACTTTAACCACTAATAGTGGAAACCTCGAGACTTTA[G/ATCTGCAAGGGGTTTAATAATGCAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTTCTTAATAGAAAATGATAAAAAATGTTTCCCCCAATAT
337	87	A G	AAAGTCCA ATGCTGTTTTT	TGTTAAAAAATCCAACTTGTTCACAAAGTACATATGTCCTATGATTTTATGCATACATCCATATACATATATCAAGGTAAAGTCCA[G/ATACAAAAAACAGCAATTCCTATGGCCAGTGTCTACAGAAAGTAAGACTGTGCMAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCAAGTGTGTCCTA

31a	44	C G ---			CTATGTATCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GJACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCATTATTTGCCACCCCTGTTTGT TAGGAA
36c	120	C T ---			CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAACCC/CJ/CCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGAAAGAGAGGCAA GG
06b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAA/CJ/CCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGAAAGAGAGGCAA GG
06a	42	A G ---			CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGGAGCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGAAAGAGAGGCAA GG
38	48	G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCCTCTCCCTCCCTTTATCTCCCTGTTTTCTTTTG/CJ/CJATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
15	54	T A TTT	TCCTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCAGGATTTGCTTCATGAATTCATCTTTCAGTTT/J/ATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
37	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGAGACCTCCAGAGAAAAATCCAAGAG/CJ/CJCTTAAACCATATTTTGTGTTTA GAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
81b	131	A G CTG CAGTCG	TGTCATTATG CTG CAGTCG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGAATTTGAATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG/JG/JA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
31a	29	G A AATT	CCAAATTCAC ATTAGTTGATG	CCCATGCAITTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGAATTT/GA/JAATTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
92	38	T C ---			TCATGAGTCTTTCTCAAGATGCTGTGTTAAAGTCCCA/T/CJ/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTAGGATATTTTGCAGACCAA

134	T C ---	CCCATACTTT TTCAGGTGAA	---	TATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTACATTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCAGTTTATACATATTTCTTTAGTTC TTTCAATTAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAITTACTCTTTACAC
40	CT A	CCCATACTTT TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGGAAA[C/T]ACCCATGTTTGTCTAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATCTGATGTGGGAAATAT TAGAAATTAAAGCGAGAGAGGCA
97	CT TTTTAGAGT	GGCACCAGCCT TTTAGAGT	TGCACAAATTG CCAGG	TGTTGTCTGACCTCCCAACAGTGTCAATGAGCTCAAGGGTTTGTATTGAGCGGGTATGGGT GGGCTATCGGCACAGCCTTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACTAGTGTGAGA TAAGTTGATTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C/T]CCATTTTGAAAAATTAAAGCTTTTGAATTGTTTTCCA ATG
b 161	CT ---	---	---	TCGGGTATTAGGATCGTTACCCCTCGATGATGGGGTTTCAATAGGAGGTGGGA[C/T]GACAC ATTACTCTCAACTGTTTCATCAGAACACTTCAACAGCG
58	CT AGGTGGGA	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGGTAAATGTG TC	CAGGAACCTTGGAGCCTTGTCTTTGTCTTCCCTCCACCTCACTCTTCTCTGCTGCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
b 134	GA ---	---	---	CAGGAACCTTGGAGCCTTGTCTTTGTCTTCCCTCCACCTCACTCTTCTGCTGCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGGTGG
a 92	CT ---	---	---	TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATTCATAAATATCTTATTTCTGCTG TCACACTAATTTGCAAGCATTCAATTTGATTGACTATTATGAGCATCGTGTCAATTCATTCAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
b 125	AT TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAC ACTG	TGCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATTCATAAATATCTTATTTCTGCTG CTGTACACTAATTTGCAAGCATTCAATTTGATTGACTATTATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
a 44	T A ---	---	---	TCCTGTATTGACACATAGTTATCTGACAGTAAATCATTTCAACATTCATAAATATCTTATTTCTGCTG CTGTACACTAATTTGCAAGCATTCAATTTGATTGACTATTATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
26	A CCGCAATAAA	GCCAAATTTTAT CATCGAGGACT	CATCGAGGACT ITGGGA	TGAGAGCCAAATTTATCCGCAATAAA[A/C]TTCCAAAGTCTCGATGGAGGCATTTCAGAAATCGGG GCAGGGGAGGCAGAGGGTGAGACAGATGTGAAGAAC

5c	103	C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAG[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGMAGCCAGAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTCACGG
5b	99	T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTTAAACAAAATATTAATATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTCACGG
5	165	T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCAATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAACAAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAATGACCAAGACACAGTTA]CCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACATAAATTCACGG
4	76	T G	CATAGCATGG ATAATATTAT ACAGAAAAA	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTATTTCTAGCATGGATAATATTATACAGAA AAAAAATTT[G/T]ACATATCAATGACTGAAAACCTACTAGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTCCAGCCTCTCAGTTTTTCCATC]A/T]TTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTGCTGTTTCAACCTCATGCTGATGGATGGTAGTCATAAAAATATGGGTGATTC AGAAAATAAGTAAATG
2	36	A T	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAAG AGAGTAAAT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAGCCGAGTTTCGATTTCACACA GTTGTCGTTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAAA CATTGTTGAAAACGAGCCACGTTTCCGATTTCACACAGTTAGTTGTCGTT
2b	61	C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAGCCGAGTTTCGATTTCACACAGTT GTCGTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G/A]TCCACGAA ACATTGTTGAAAACGAGCCACGTTTCCGATTTCACACAGTTAGTTGTCGTT
3	187	G A ---	---	---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG]G/G]GCAAGTTAGAT CCCACCCTCACTATTGAGAAGCTAAAAGTGAAGACTACTCATTTCTCAGTCTCCTTGCTG
1	52	A G	TTCTACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTTCCCTAAACCTCCTGTTCCCTCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTTCAAGAGGTGAG TAATGCTTGGT]C/T]TGTCTGTGCGGTATCTGCTCCAATCAACCATTCACATTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG
7b	148	C T ---	---	---	

37	165	CT	---			GAGTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAAC TTCACATTCAGCAGATATT CTTTCATGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTGTCATGATTTCAAGAGGTGAG TAATGCTTGGTACTTCTCTGTGCGGTAT[C/T]TGCTCCAATCACCCATTCACATTTTATTTCTATTAT GCTGAATGAACGGTTATATTACAG
33	53	GC	---			GGGTAAGATCCAGAGCCACAGGTGAACCTCGCGGGTATTGAAGTCTTTGGGCCA[G/C]GCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGACTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACATTTTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAGGAATGAGG
41	80	TC	AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGCTCAAGAAAAAATAAATTGAATAATTAAAGCACCTCTTAATTAAGCAT CTACAAGGTACTTAT[C]CACTGTTCTGGGGTTTCAATCCTCTTACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGCTTTT CTC
150	45	TG	TGTCACA		CT	ATAGGACAGTTTTTCTCCAAATGACTTATTCTATATCTTGTCACAT/GIAGAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGTAATATGATGTAAGACTA TTTTTACTGGCCTCTTTTATGTCATAAAACAAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGCTCCCTCTGGTACTAGAAATAGTCTTTATAGAAATATGTGTTTAGAATAAGCCACA AATTATCTATAAACACACAC[C/T]AAGGAACGAGGCTCAAAAGTGGAAACAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
161	88	CT	---		---	GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTCAAGTGAAGTATGATCAATAAAGACATGCAAAACCTTTTCACAGTCTTGT CCTGG[G/A]AATATCTCACAAAATTAATTAATAATGGCATGGACTTTCTGATTTAGCCTGACAGG ATTGTCCTTT
166c	141	GA	TTTGCTGG	TTTTCACAGTC	AGTCGCATGCC AATTTATAAT	GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/T]ATTCAAGTGAAGTATGATCAATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATAATGGCATGGACTTTCTGATTTAGCCTGACAGGA TTGTCCTTT
466b	80	T	CTC	GACTTCTGGG CTATGAAATA	ACTGAA	TGCTTTTAAAAATAAATGACCACCACTGACACCATAGTCTGCTCCATTTGCCACGCTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT[C/A]TTCTCCTTCAGAAAGACACTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGTCCTTTTGATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTGGCCTAT
814	104	CA	---		---	CCTCTAACAGAAACCTTGACTCTCAACTCAAAAATACCCTTCTCTAATAATTTA/GIAGTAACCA AAATATTCTTCAATAAATAATTAATCTTTTAATTAGAAAGAACACAGTTAGAGGTAGTACATTCA CCACC
1720b	55	A/G	---		---	

20a	47	A G	---	CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTTCTCTA/GIATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
25	123	A T	---	CACGCTAAGGCAGGATGGCTTATGAGATACCTTTCGATGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGTGCTTATGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTACCAAGGGTTAGTTGCAAT TAAGAAATGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTATCCACATG
18	74	C G	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTAGATGTTTTCACACAGCCATCTTTCTTTCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCA
43	91	T C	---	TGAGGCTATGATTGCAGATTTGTAGTGAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC[C/JATTTTAAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTGTCTCCTATTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTCTTTAGGGA
31	39	T C	---	AGGGCCTTACAGATCCGTCAGTCAACACTGCTCTT[C/JAGTGAGCCTGTGAACCAACCAAGAC GGCTGTGCATCAGTGTGCATCTCTCTTTCCGGACAACATCTTTAAAGAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCCAAATAATCTTTTAAATAATCTTTATAGCCAAATCCAAT GTGCTGAATAATCTGCCAAGCATGTCTATCTACACAAAAGGGATTGCAAA
17b	84	C T	---	CTCAGAAATTTACAGATCTTCCCCAAATGTGCATGATCTTGTCTCAACATCTCTATTTTCTCAAC ATTTATCTAGCCTGT[C/JAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
17a	83	A T	---	CTCAGAAATTTACAGATCTTCCCCAAATGTGCATGATCTTGTCTCAACATCTCTATTTTCTCAAC ATTTATCTAGCCTGT[C/JAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
15b	115	C A	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTCTTGAGCTGGCAGGGGGAGTTCAGACA[C/JAGCCAAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
15a	42	C T	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGC[C/JACCTCACCAAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTCTTGAGCTGGCAGGGGGAGTTCAGACACAGCAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
33	146	C T	---	CCTGTAGTGCCAGAGTCCATGCTCTTGGCCACATGTTAGGTGCCTCCCAITTCCTTTGTCTTGA TTCCCCAAACCAAGGTTCTACCCCAATCTGATCAATGTCTAGTAGGTCTGGCTGGTCAAGGTAA AGCATTATGA[C/JTAGACACAAAGACAAAGAGGTAAAGTTGCTGTCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

19	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G A	A T A T C A G T G G G T T G A G T A T A C A G C A A T C T A T T T T G T T T A T T A T T A T G T G T G C T A T A A A T C A A T G G T T C T A A C A T T C A A A T A G A T C T T T T G C T T C T G C T C A G A T G C T T T C A A T G A T G T A A T G C T A T G T A G C A A A T C T A T T T C C C C T A A G C A G A T A A T C A A G G C C T T C T A C C C A
2	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T A C T T C A T T G C A T C T T G A C T C G T A T T A A A T A A A T T A T G T T A A C T G G C T C T G A A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G C G A G A A A A A A T C A T G A C T T T T T A A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C T A G G G T T C C G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
3	39	T C A T A A A T T	T G T C A T C T T G A C T C G T A T T A A	A A A T T C T T T T C A G A G C C A G T T A A C	T T A C T T C A T T G C A T C T T G A C T C G T A T T A A A A A T T A T T C J G T T A A C T G G C T C T G A A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G G C G A G A A A A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G G T T C C G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
4	170	C T T T A C A T G	C C T T T A G A T A T A T T G T A T T G T	A C C T T T C T G A A G C C A G A T T C	T C T G A G T C T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A T T A A T A A A T A T A A T T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G G T G A C A C T C T G T T A A T C C A G T A T C C C T A C T C C T T T A G A T A T A T T G T A T T T T A C A T G C T T A A A T C T G G C T T C A G A A A G G T A G G T G T T T
5	54	C A C A G G A A G G	G T A G C A G G A T	C A A A T T A T A T T T A T T A T	T C T G A G T C T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A A T T A T A A T A A A T A A A T T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G G T G A C A C T C T G T T A A T C C A G T A T C C T A C T C C T T T A G A T A T A T T G T A T T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T A G G T G T T T
6	289	T C T C T G T C C C	T C T C T G T C C C	A T T C T T G T T G T A T T G A A T G G A A T T A A	C C A G G G A T T C T C T G T C C C C A A A C T C T A T T C J T T A A T T C C A T T C A A T A C A A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C A C A A A G A C A C C C T T A T A T A G T
7	119	A A T C T T T	T G G C A C T T A G A A C A T A G T T T	G C C A C A C A C C C C T A T G G T	A A G A A A A T C C T T G T G G C A C T T A G A A C A T A G T T A T T C T T T A T J A C C A T A G G G T G T G G C T T A T C T T T T A C C T G G C A T G G C T T A G G T C C T G T T A A T T G G T A T C T T T T G C C A C A A A G A G A G T C T G T T C T G A C A G T C T T A T G A T C T C T A T T T A A C A T T A A C A C T G G T C A G A T G T T T A A A A C T T G T T G A A C C T G C A G C A G C A A C G T G T A C A A C T A G T A G G G T G T A A A T C A G A A G C A T C T A T A T T A T T C A C C A G T C A C C C C T G G A C T A T A G T C T G T T G A T T T C T A C C T C T A T T C T T A T T C J T A A A C T T T T G G A T A C A T T C C A A A A G C A T C A T G G T C A C T T C C A G T A T A A A G G A T G T T T A A A G C C C A G C C A G T A G T T G T G C A C A A T T T G G A G A C A T T C T G A C C C C A A C T T A A A C A C T T C T C C C A C A C T T A C
8	572	T C T C T T	T T	---	A A A G T T A A C A C T T C A G T T A C C A G G T A G A T T G A G C A G A

38	31	C	T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACCAGGCTGTGTTGCTACCCCTCTTAGAGAAATAAATAATATCTTT
				AGGCTCTGTT	ATTTATCTCT	GAGATAGGGAGGAGCAGCCTGAGGACAGCTGGGTTTTGTTCTACCCACTGGAAGCAGAAATATCC
					AAGAGGGG	TTCAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCCTTTCAGGG
31	32	A	G	CTGTCTCAGGT	GGGAGTTAGGA	T
				GTCAAGAAGTT	GTCAAGAAGTT	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCAGTCAACTCTTGACTCTCTAACTCCCATCTCGGTG
				GA	GA	TCTGCTTCCCAGGGGAGCATCTGACACAGCCTTTTGTCTGCTTGACAAACAGAACATTCGAGAAG
						TGATGCTGCGTGACCTCCAGGATA
				GTACCCAGA		AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTTCTTTTTCATATT
				GTCTTCTAATA	TGCGGCTTCCA	TTCCAAATTTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT
146	A	C	G	GTAGCT	GTAGCT	CTAATAGCAAACJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTTCTTTTTCATATT
				---	---	TTCCAAATTTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAAGTTACCCAGAG
						TCCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
				GGGTGCTCAAT	AAAATCTGTT	AGCGATGAAATTTATATGTTATGCTTGCTGACTTAGCGGGTGCTCAATAAATATTTCTTTTTCATATT
				AAATATTATT	GGTGAAATTC	ATTTTCCAAATTTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT
				CTTTT	TAG	CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
						CGTTGGGAATTTCTATCTCACCTAAATTTATGCGTGATTTAAATATACATTTTAAACAACTTCAAA
				CAAACCTCAA	AAATCCAA	TTGCTTTAAGTACTTTTACJGGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTCTTTTCTTAATA
				ATTGCTTTAAG	GTCAAGGCTTT	AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTTATCTGATATCAGCATCCCTT
				C	C	TATGTATT
						CGTTGGGAATTTCTATCTCACCTAAATTTATGCTGATTTAAATATACATTTTAAACAACTTCTC
				GGGAATATTTC	GCAATTTGAAG	AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTCTTTTCTTAATA
				TATCTCACCTA	TTTGTAAAT	AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTTATCTGATATCAGCATCCCTT
				AATTATG	GTAT	TATGTATT
				CACAAATGTA		GTGTGAAACTCCAGTATCATTTCCCTCAAACCGCTTAAATCAAAATCACTTTTCTTTCTGTGA
				ACAAGAATTG	CCATGGCTGTA	GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCAAAATGTAAACAAAGATTTGATCCTATTTCTACTGGG
				ATCC	GTCCAGT	ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAAACAG
				CAAGTGAATT	TGCTCTTTCA	
				ATGACCAAAA	TTTGAGGTTTT	TGACTCAAAGGAAACACACAAAAAGTTTACCACAGTGAATTTAGCCAAATGAGAATGAAAT
				TGAGA	T	TTGTTAAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT
						ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTTCTTTTCTTTTGTGTCCTTA
						GAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAATTCACCTTTTCT
						CTGTGGATGATCAGAGTTCTGCTCTCCCAATCCAGAGGAGGACTACTATTCACCCCATGGGGTCAT
						AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC
56	59	T	G	---	---	

						CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAACTGACTTGAAAAAATAATTAAGCCCTAAAGTAGTGCCTTTTAACCAAGAGTTTTTCATTCCTTTTTTTAAAAAAGAGCAGACAT/GJTTTATCAIGTGTTCTGATAATTTTTTTATATATTTTGAATGAGGATTTTAAAGTTAGCAT
154	T G	TTAACCAAGA GTTTTTCATTC TTTTT	CTAACTTAAAA ATCCTCAATCA AAATATAA			CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAACTGACTTGAAAAAATAATTAAGCCCTAAAGTAGTGCCTTTTAACCAAGAGTTTTTCATTCCTTTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAATTTTTTTATATATTTTGAATGAGGATTTTTAAAGTTAGCAT
95	A G	AATAAGTGAA AGTAACTGAC TTGAAAAA	AACTCTTGGT TAAAAAGCAC TACIT			CAAGTGTCTTGACCTTGATAGGTC/GJACCGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAGACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCCCTTTGGGTTTACCACCTAGGGGTGCATAAAGAGAGATGGGAGACAGTCTCAATCTTGCTCTAAATAATTCAAAATAGCCATGGGTTGGACAAAATACAAGGTTAGTGCTCTCTAACTTTAATGGGCATA
5	25 A G	---	---			AATAACCTGTGGCACAATAAGGCAATACTGAGCCCATACAGAGTGTTTTATGTTAATATTATGAAA
16	133 C T	TGCCCTGTGC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA			AAAGTCAAGAGAAAGATGATAGTCTGCTAGAATACTTGAAATCTGATGCCCTGTCCAAAGG[C/T]TGCTCTACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAAAGGG
						GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAAATATATTGCTCCCAATGATCTTTCTGCTCAAGAGAT/AJTTTTTTTAAAGTTATCTACTTATTTATCTGCTTTTTCAAAAAGAAATGTGAGAACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATTAATAAGTAAGAAAAAGAAAGCCAAATTTGGGC
75	77 T A	A	AA			TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGGTGGTGAGGTGAGATTCACTTCTTAGAAGCACTGGCTATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTGTTCAGTCTTGCAAAATGCTTTATGAGTTTTTC/GJTTTCTCTCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCTT
144	A G	TGCAAAATGCTT TATGAGTTTC TGAATTCATCC AGAAAAACAG	GGCATTTTGTA AAGGAGGAAA TCTCTTTTCTC TCTTGTGTCA			GTGAATTCATCCAGAAAAAACAGC/T/CJGAATGACAAACAGAGAGAAAAAGAGATAAAGGTTTTTGTATACGACAAGTGGCTCAAGCAATTTCTCTGTCCTCAGTGCATGGAGCAGTG
3	23 T C	C	TTC			CAGGCCCAACTCTGTCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTGTATGTGCCCAACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTTCTAGT/CJGGCTGCTGGCAGTGCCTTCCAGCCTGCTGCCCACTAACTAA
19	115 T C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC			CAACCAATTGAGATTTAAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTTATTTATGTGGGAGTTCTGAAGATTCCCATGGTAAATAGTATTCCCTCTCCCTGCTTAGGTTTTGAAGAAAGTTGAA
21	40 A G	TGGCTCTGCTA CTTGCCA	ATAAATAAAT CTCA			

88	T C ---	---		GCACACGAAATTGATTAAATTGGCTGACTTTGAGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAACTTTCACCTTTTTCATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAAAGCTGAGGAAATTTATTCAGAAG GCAACATC
80	T A AACTT	GTAAAAGGG TGATAACATAA TACCTTT	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTGGCTGACTTTGAGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTTTACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAAAGCTGAGGAAATTTATTCAGAAG GCAACATC
2	C A ATTGGTCACT	GCTGTGCTTC CTTTAA	AAGAACAATG CATAACAGAA CTTTAA	ACATGTAATTCCTTTAGGGTCAGCCTTCCTACCCCAAGAATATCCCTGGTTATTGCTGTCTTC ATTGGTCACTTCATTAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTAAACTGTC
6	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA		TAGCTTTTCTTTGTACGAGTGCATAAAGAATTACCACICTGTACATTTTGTAAAGATAGCACAG AGAGAAGCAATTACAGGGCACAGCACAAACATGAGGTGTGTTTTCTGTATGTACAACTC(NT)CCAA CCATTAGGATTGTCACICTCATATATAGACAGAATTCAGTGGTGGTGAATTTGAATCCACACATGGA ATAAGTCTA
5	68 C T ---	---		GAAAWAAAGTTTAAATTGGATTGCTTAGTTTGCTTAAATTTGACCTACTTTTCAGATTATTTTAGT [C/T]ATTTTCTTCTATATATTTCTTGAAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATTCCACCATGT TTT
89	G A AGAGAAA	GAGAGAATAT TCCAAAAAGT TTCT	GGTCTCTAAT TTTCTACACT TTCT	ATGAAAAATGCATTAGAAGATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAAATCTC
18	G A ---	---		ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAAATCTC
136	G A GGCTGG	CATACCACCTGC AGTTGTGA		AGCCACAGTGGAAATCAATTTACACTACCGAAATCAGCAAAATGCTAAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACCTATTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAATGCTTTACACAGGCTACTGG AAAGCC

25	C T A	G C C A C A G T G G A A T C A T T T A C	T T T T A G C A T T T G C T G A T T T C G	AGCCACAGTGGGAATCATTTACACTA/C/TJGAAATCAGCAATGCTAAATGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCAACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAITGGCTTTCACAGGCTACTGGA AAGCC
75	39 C T	T T T A T G C C A T A T T A A T T C A T T A T C A C T C	C T A G A T G T A T T T G C T A A G A A A A T A T G A T G	TTGCAAGTTTGTTTTATGCCATAITTAATTCATTACACTC/C/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATCTTGGCACGATAATCATTTATCATTTAGACATTGCA GGAACCACTATGGATGGATAATGTGTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATTGTCAAGTGTGTC TAGTACAGGAATCAAATTTGGACTATGAACA/C/CJGACATAGTTGCTAAGGATAITCCACAAAATTAT TTCATGA
26	165 A C	---	---	
78	62 A G	G C A A G G G A G G A A C A T T T A C A	C T G G T G A C A T C A G A G A T G G A C	CAGTGGCTGGCTACTGACAAAACGTAACTCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/C/GJG TCCATCTCTGATGTCAACAGCAGGGGCCAGGAAGGTTGATCTGGAG
89	21 C T	G G G A C A C A C T G C T C T A G A C C	T T G A G G G A C C C T G G G A	TGGGACACACTGCTCTAGACC/C/TJCCCAGGGTCCCTCAAAAGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACCGACAGGCATCAGGGCCCTAGTCCCTCTGGGACAGTGAAGGGCCCAOCC
110	58 C T	C A T C T T C A T G G G C A G G A A T T	C A A C C C T A A G A A C A C A G A A A T G	ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAGCATCTTCATGGGCAGGAATT/C/TJCATTT CTGTGTTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCTCTAGAAGTCATGCAAGAGAAATGATGA
128	23 T C	---	---	GGACCAACAGAAATTACTTGGCA/C/JAGGGTTTCTTAAACATATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATAACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTGGATACATTAGGCTCATTTAGGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
132	91 G C	C A T T A A T C T G C A G G C T C T C C	C C T A A C T G C A G G T G A C T T A G A A A	TATGCCTTCCCAAGGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC/CJG/TJTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAAAGGCTGCTCCGTGAATAC TAGTTCGG
134	96 C T	A G A A T T A A C T G T T C A A A A G T	T G G C C C T A T A A A A T T G G T A T T A A G	GATTTGAGTATTATCAAAATTTGCCCAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACATA AAGAATTAACTGTTCAAAAGTGTGTTAAT/C/TJCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCACATACTCAACTAAATTTCTAAAGTCCAGT
137	24 T C	---	---	GGATGATGTTCTGTGGTCCCTTAT/CJAAAGCCTCTTGATCCCAAAATGTGTAAATTTATTATTCT TGGTATTTCTGGCTTACCATAGTACCTGTCAAGTGTCCACCCCT

3b	77 T A	---	---	CCTGAACACCTGGAGACTCCCTCCCTGGACACCTTCATCTTGCTGGAACCTTGCCTGGAAATGCTC TTCCCTCTT/A/GAGCTTTGCTTGCTTACCTTTCTTTTCCCTTAGGTTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGGTGAACACAAA
6a	50 A C T C T G C T G G	G A C A C C T T C A T	AGAGCATCCA GGCAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTTGCTGG/C/CJACTTTGCCTGGAAT GCTCTTTCCCTCTGAGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGGTGAACACAAA TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAACATTTATTTCTCTAAAT TAGATTTCCACCCCGACACTATTTACACAGAACAGCATGGAGCAGTTTGGAGCTGGCTCTAGA GAACCTACTTAAGGACAGTGGTTTCCATCTGCTTCCA/C/TJAGAGATCTAGGGTGTCTTTGGAAACC ACCTTGG
6	175 C T	---	---	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTGCGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATAGATGTGTTAAGTAAATATATTAACATGGTA CA/G/AJACAACTTCAGTTTAACTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATG TGA
1	136 G A G T G T A A G T A	G C C A C T A T A G G	---	CTGATGTTTGGGAAGCACTGCTTACATCTCTAAATGTACGACCCCAACACAGAGACCCCG/G/A/JT GAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTCCCTGGTGCATAGTAGACACT
10	62 G A A G A G A C C C C	C C C A A A A C A C	A T T G A C T A A G A	ATGGATCTGCTCAATTTATAGTCCAGATAACAGCCCTTCTCCCGCCCACTTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTTGACCTCATAAAGTATTTT TTCTCTTCTGTGTTTGTGTTTCTCCCTTCTTAAAGAGATAGT/C/G/AJCCAGAGGGCAATTCGACTTTCTGT AGCCACAAGATT
34	177 G A T A G T C	A A A T T C A A C C	G C C T C T G G	ACAACACAGCAAAATTC AACACAGATCTATTAGATTCT/AJACCCCATCTCAAACATATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
37	37 T A T A G A T T C	A C A G A T C T A T	T G T G A T A G T T T	CAAGCACACATTCAGGCAGTGGCAGGTAGGGAAGGTGGGCAACTTCGCGCAGCAGAGAGGGAAG AAGTTCAAGACCGTTGGGTAGGATAAGTGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGCAG ATAAAGA/G/AJCCAAGCCCTAGTTTGAAGTACACTGTGGGGATTCAAG
38	140 G A A G A T A A A G A	G T G G A G T G G G C	T C A C T C A A A C T	ACTCCACCAACAGTTTGTGAGCCCAACCCCTGCATGGTCTTTCTCTG/C/JTJTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
75	47 C T T T T C T G	C C T G C A T G G T C	A T G A C A A T G A T	CTGCCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCTTACATG/AJCAAATGCTC CTTTTAAGTCCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGA
02	55 G A A C A T	A G C A T A T T C A	G A G G A C T T A A A	

3	33	C T	CCAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCGTGTTCTCCTCAAGTTGTAGCATTGAGAGTGCCTCTTTAGAGGTAGTTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACCTCTCTCCAAACAAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGACACATAATTAATCCCATTTGCCTAAAAAGACCAGG
3	70	C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAAACACAGAAATTTAACAAATGAAATTCAGCTACTCTTCTTAGGCCCATCAGAG AACTC/TAAGTATGAGGAAATTTGATGCCATGTGAATGGAGAAACAGACAGGCATATATATGGAG AATTACAGTTTACCAGGGACACAATCCCATCTCCAGAGCCATCTGTAAAGAC
4b	109	GA	---	---	CATGCTAGGTAGTCTGATCATGAAGTTGAACAACTTAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCAC/AG/GTATTTTATGAGGTGGTGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
1a	90	A G	AC	CAACCATCAAT TTCTCCCA	TTTGACCCCATACATGAGAAATAAACCATAGAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCT/CTTGGAGCAGGGTCAACCCAC
2	79	C T	GGATGTCT	GGGTGAOCTG TCCTCA	TCACGGCAAGTTCTGCAGCAGTGCCTTGACTCTGCCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAACATCT/GC/ATGGAAGGCTGCCTGGATGAGGTCAAAA
0b	146	G C	CATCT	TTCCAT	TCACGGCAAGTTCTGCAGCAGTGCCTTGACTCTGCCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCCTGGATGAGGTCAAAA
0a	78	T G	ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTCAAGGTAAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTTATGATGCACCT/GT/CCTTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAAGACACAAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTCCAAAAGCCTTTATGCTTAC
8	125	G T	---	---	AAAGCGATGTTGAGATACCACATTCCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/C/JAAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAITCCAGAAATCTCTCTGTCAATCTTAACCTTGTGACAGTGCACAG
7	67	A C	---	---	TCTMAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCCCTCAGTTATGTATCAAAATGA AAAACT/C/JACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCTTATTTTAAATGAAAA GATCTTGGGCAATTAACCTC
5	72	T C	AAAC	GGCTCACCAT CAITGTTTT	

19	51	CT	...			GAAAAGCAGGAAGCCAGGAGGACAAAACCTTTGAAAAGCTTTTTCAGCAC/C/TTCGTGGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGCCAAATTAATGAATGTGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACAGAGGGTGGGGTGGGAGGTGAATAAC
46	116	GA	...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGAATGTTGTCTTCATCATCTCTGTCTGCG/A/GCCCCAGGATAAAGCA GGCA
37	49	TC	CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTCCTGACAA/T/CJCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTACTTGAACAAAGACACAGT CATTAAAGTGGAGAACCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
38	25	AC	G	TGACCAATGTG TTTAGAAGCA	TOGTCGGTGC CTCTOC	CAATGACCAATGTCTTTAGAAGCAG/A/CJGGAGAGGACACCCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGAGCCACAAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
01	114	AG	...			GGACATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTGCTTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAAGTG/A/GJ/TATCATGTGCTACACTGC AGTGTATATGCTGCAT
14	99	CT	GC	TGATCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACCTTACCTGAGGAACCTTTTAACTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC/C/TJACCATCCTTATGCTTCTAGACCTATACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTAGGCTA CAAAAGAG
19	33	GA	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/G/A/CATTTGTTCTGTTATTGCTGTTTCACAGAT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGTGTGCAAGGACGAGGGTTC
91	84	AT	GT	TTGAGGTCITA GTCAATGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTTGTGCAATTTATGCTTCTTATGTAACACAAATCACCACATTGAGG TCTTAGTCATTGCATG/A/TJTGATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGIGT ACATTTATTGCTAACAGCAG
60	117	AG	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGTTGGCTTCAAGATGGTAAT ATCTGTCCAAAGTTTGTGCTTCTTATGTAATTTAGCAACAATATCAACAGAA/A/GJGGCTATATTAGAAA ATTCTACCTGCATCCCTGGATCTGAACGTTCTTCATGATACT
68	32	AG	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAATTTGATACAAACA/A/GJTGCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

7	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTCGGATATACCTTCCAAATGACTAGTATGAATAAGCAGCGTATTAAATTTACCTATTATATTT ATT/CJ/CATCATGATTTGCTGGCTCTTTCCTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCCAATAG
9	51	A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACCTCCCCAAGTTAGTCAATATAAAAAA/CJ/CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
3	24	C T	CTGTCACTGGT CTGGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACGTGGTCTGCCCTGTC/CJ/GGCTCTGTTCTCTGTTCTTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
3b	117	A G	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGTGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
2a	94	G T	TCAATATGAG TCTGTGAAAC AGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGTGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
5	68	G C	TGCTCCCCCAT CACCT	G	TAAATGCTCTGGGAGATAATAGGAAGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CCTACACAACCTTGAAGTAGGCCCATCCAAACACTGTGTAGAGAGTAACTGTGAC ACAGCCTCTTCAATGGCACAAATCAAAAGCACACAGTAAAGAGCAGAGGCAAAATCTGG[C/T]CTCAC CATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
8	57	C T	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGACCGGAAATGG GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
5b	71	G T	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
3a	58	C T	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTGGATGCCACTTCTGCTGTCAOCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCTCTGCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCTGTATCTGTTACAGGCC[C/J]GAAATCTGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
7	158	A G	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGGCAAGTCTGGTGTGCTAGGTCAGAGGCAGCG ACCTGAGGGACACACAAACCAGTGGGACACCAGGGTACTTGTATCACCT/CJ/CTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAAGACTCCTTACTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACTTGGGA
6	117	T C	

10	110 A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTTCTTAAAAATGGTGCCATAGTACTGGCTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTACAGTACTTTGCAATAAGCACCATGTGGCATCCAGTGGATGGCTGCATTGTCCAGTC AAATGAGACAACCTCCTAT
12	226 T C	---	---	AGCAAGCATCTGGCAAGCCCTCGGTGACCAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATCTCTGTACACA AATACTTTATGGGAGACAGCATTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCCTCCTTGCTAGAAACCAATTGAT
15	105 G C	AG	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCAATTGAGGAAGTGTAAAG/CJAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCACTACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
18b	99 C T	TTG	AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAACGCCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJTCCTTGTCTTTTTCCTTCTCTCTCTTTTCTG CCCTCTTTTAACTATT
18a	38 G C	CTACGTTGT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAG/CJAGCAACCCAGAAAAATTAAACGGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTCCTTCTCTCTCTTTTCTG CCCTCTTTTAACTATT
16	69 T A	AGCAGTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGCTGCTGAAGCAGAAAGCACTGTGA CT/AJCATTTATTAGGCCATCTCTCGCTGAAGCCCTGCCTACAGCAATTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCAACTATTGACAAGATTCTCCTTTTAAACAA
12	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTGGGAAAAGGATTGTGATGATCATTG AATCGTTTAAATACAGAATTAATCTGAATACCTGTGTGAATCATTTGCTTTC/JACCATGTACA TATTATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
16	61 A G	CT	TGG	TGCAAAAAGGAAAAATGATAACCAGGACTGTGTTTCAAGCAATGCTAGAAAAATTATGCTA/AJ/C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTTGTGCTTAAGTCTCTATTCA ATTACCATTTATCGGGGTAAATAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
7	77 C A	GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG/CJCTTTCATCTGCCCCCTGGTGGGTTTTCAGTAACCTGCAACATGCTTTGCTCC CGGATGAAAGATACCCCTCTATGACTCAGCAATTCACACTCCTAGGTATGCCCTTAAACATGGGTG GCAAAAT
19	50 C T	TTCCGAATG	AATCATC	TCACCTGTTTAGAAAATTTCTTCTCTCAGTGAGACCACTCTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAAATTTGTAATTTTTTAA AAAACTCTCCCAATATTG

					TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACTGCTGTTATGCTCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACTGTGCTTTAAAGTGTGAAGTATTA ATTAGATTTCTATTTTGATA/C/TTTGATGTTCTTCAAGAGGAAAAATTTGTGAAGAGGATTCCTCAAT TGCATTTCCATTGGC	
155	C	T	ATTAATTAG	CA	TCATTGACITTTTAGAGTCCCTCAGTCTTTATGCTTATTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAGATACTAGAAAAATGC/C/TTGAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC	
113	C	T	AATGC	GTTC	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAACTCAGTGCATAGATCATCTTCTAAGTTC/C/AG TTGAAAAAAATTAATGCCAAAATTTTAAATTTATCCAAACTTTAAGTCGAGATTATAATTGATATTTT AAAAAACTATATTGAGCTTTCTTAAAAAGATGGCGTATCACTCTA	
65	A	G	TTCC	ATAA	CTTACTCCAAAGTGTTTCCAGAGACCACTTCATTC/C/TTTTGGATTATGAATAGAAATAGAAAAGAGT AGGTGTTATTATTCCTCTTTTACCAGGTGAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA	
38	T	C	CACITTCATTC	CAAAAA	TATAATGTTTTTGTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAGGAAAAATATACATATGGGTGATAATGGGCCCTGTTC/C/CTCTGGCATA CATATAAAGGAAGGCTAA	
121	G	T	GCCTGTT	GA	TATAATGTTTTTGTCCATAGTTGCCATAGACTAGGTTATGTCC/C/AG/CACATGAATAAACAATCTTAT TTGCCATAGACCATATGTATAT TAGGTTATGTC TTTCCTTCTTG	
3a	43	A	G	C	CATATAAAGGAAGGCTAA	
					TTTTTCCATTTTGTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGTTAAT AATATAATAATATGATGTTATATTAACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATAT/C/CGGACTCAITTCCTTTTGTGATCTATTTCTAGGTTATTTGCAGCCCGAGATCTACCCAGG	
7	139	T	C	GTAGCAGGT	C	AAATGAGTAACCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA/G/ATGAAT AAATGAGTAGTGGAAITGCTTGATAACTGGAGTAGTGCTT
3	56	G	A	AAAGATAACA	CA	AACATTTTTAACCATGCTACATTTACAAACACTGAAAAGACAG/G/AAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACACTGGAAAGGAG
3	44	A	G	---	---	GCCTTTTGTAGTTTAAAGTCTTTTGTAGTGTGCTCTTTTTTTTCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAATAAGCGCTTGG/G/G/ATAAACAACATCTTC
7	93	A	G	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCTG/A/CCTGCTATGGTTTGTGTTGAAGCCACATCCACT GAGGTATTTCTGCTGCATTTCTATATCACTCAGCTTCAGATCCACTCCACTCAACTTGCAG
5	29	G	A	---	---	

2	232	C A ---	---	GGATAATCAGTACAAATATGGGACCTTAAACTGCTGTGATGCAGGAGTGGGGCTGGCAGTG CCGAGGCAGGGGAGGACAGTGGGACAGGGATGCTCAGTGGTGAGCCACAGCCCTGGGCTTGGA TGGGCGATGGGAATGACAGGTTCCACATCATGCACAGAGGGCTGTAGCTTGAGTCCAGACAG GGCTGCCACATTGGTGTGCCCCCGGCTA/C/A/CTGGAGATGTCTCTAAAA
4	138	C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAANAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAAT/A/G/AAACCCAA CT/C/T/TTTCAACCATTTAGTTGATTATCATCTGGATTTCACCTCAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAAGGAACAAT
4	123	A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAANAATCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAAT/A/G/AAACCCAA TTTCTCTTCAACCATTTAGTTGATTATCATCTGGATTTCACCTCAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAAGGAACAAT
5	74	C G ---	---	TGAGTCTGAGCAGGAGTTCAGCCAGGGCCAGTGGGAGGGGTCTGGCCAGTGCACCTTCGGGGGCG GCATCC/C/G/TTAGTTTCCACTCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATTCTTTGTTTCCCTGTTGA GTTGTTCAAAATGTTCTTTTAA
3b	42	T C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/C/CAACAGCAAAACAAACCCACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTAATTTTATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTATTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
3	56	A C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA/C/CAACACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTAATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTATTGTTTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
17	41	G A O O O C	---	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCTCCCG/A/TGAGGACTGGGTACAACATCCA AAAGTTCAACAAACCCAGAACTGTGTCTCATGGT
38	180	A G ---	---	TATACCACCTCCATTTGATGATGGAATGCTGCTGTTTCATGACCACTTTATGGCTAGATGGTTCAGAA AGCACCCAGTTTCATGATAGGCAGTTTCAGGTCAATATGTTGACTTGTATGACCCAGAGTCAAAACATTTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/A/G/JAGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGTCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
05	26	C T G G G A A T C T	---	GGTCCACGAATTTGCTGGGAATCT/C/T/G/TTTTTCTTTAAGACTTTTGGGACATGTTTGACTCC CGAACATACCGACCGCTCTCTGTTTCTGTTTCTGGTGG

46	G A	TTTGTGTTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAG/GAATGAGATCAGTTTGGGA CACTCTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAA
78	A G	AGTGCACTTGGGGAAAGGCTCCAGTGTATCTGGACCAGTCTCTTCACTTTTTCAGTGGGACTCTT GATCCAGAGA/GAGACAAAGCTCCTCAGTGAGCTGGTGATATCCAAAGACAGAACCCCAAGTCTCC TGACTCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCACTCCAC CTATTCTCTGAAAATATTCCTGAGAGAGACAGAGATTAGATAAGA
43	C G GCCATC	GCTCCTCGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGAGAGGCCACCCAGCCATC/GTGAACCCAGGAGGCCAA CTATCCCAAATATACCTGGTGAATATACCAAATCTGCATCTCCAGAGGAAATAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
53	A C TT	TCTACTTTCTG OCTTGGGT	AGCAGCCATCACATGATCTGTTTTCCACCATTCTCACTGAAGACACCATTTATACJTACCCCAAGGG CAGAAAGTAGAATTACTATTCATTAATGTTTGACACAAATGGAATTGTC
293	T G	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAATGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCTTATTTTCTTTCCATTGCT TATCTTGAGCACAATGATAATCAATTATACATTTATACATCACTTTTGTGACTTTTCCAAAGCCC TTTACAGCTCTGGCATTCTCTCGCTAGGCCGTGAGGTAACCTGGAT
38	A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTAAAGAA/GAAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
249	C T	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGTGGCAGGAGACCCCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTTCATGCT GTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTTGCTT
157	C A	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGTGGCAGGACCCCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAGGGAGCC CCAGGCTGGAGCAGCATGAGGGC/A/CAGCAAGAAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTTGCT
34	C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTCA/CJTGCCAGCTCAGCCCTACACAGTTTCCACC TGGAGTTTCATGAAGGGCAAAAGGAGTGCCATGCAAGCTGTTTAA
61	C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTGCTGGC/CJTTC CTGTCTAGTCTCTCTGTAGCCAAAGAAATGAACATTCCA
93	T C	CCCTGTTCCTCATGCTGAOCTGTGTTTCTCTCCCAAGTCATCTTCTGTTCACAGAGGGTGGGCTGGAT GTCTCCCATCTCTGTCTCAACTTTAT/CJGTGCACTGAGCTGCAACTTCT

32	C	CAGGTC	CACTG	CCAC	GTGACCTGTGAGGTCAGGTC	CCAGATTGAGC/GCTGCTGAGTGGGCAAGTGTGTCAAAGGGGG
		GATTGA	ACTCAGAC		TGCCCCCAGGAGATGAGGCTGAGAGGAGGAGTTGAGGCCGAAGATCA	
		CAATAAACA	GCTCTCAGAAC		TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCAATTCAGTAGTTACTGAAAGAAAACCTCTGCTA	
		ATGCAACGTTT	CAAGATTAGA		GAATGATAAATGTGATGGTGTCTATACTCCAAATAACAATGAACGTTCC/TGCTGATTCTTAAT	
120	T	C	AATC		CTGGTCTGAGAGCCATTGGTTTCAAGTTGAGTGTAGCAATCCCATACCAGCT	
		CAGTTCAGCT	AAACAATCTA		TCATTCTTTTGGCCCTGCAGCATGTCTATGCTCCAGAAATTCAGCTTCAGCTTAACGTGACAGATTC	
		TAAGTGACAG	ACCAGAAAGCT		GTAAAGCTTTCTGGTTAGATTGTTTACATTTGGTGATCATGCTTTTCCATGTGTACCTGTATAAT	
65	T	A	TTAA		TTCCATCATATCTCAAAGTAAAGTCA	
		CTAAGCATGT	CCCAATTTTA		CAAAATCTTGGAAATATCTCAAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT	
		ACGTGAATTTT	TTAAAAGTTTA		AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAACITTTTAATAAAATTTGGGGTGTGG	
91	T	G	CATCTAT		GAAGATTAAAGGAGGTTGCTCTGTGGTCTCTCCCTCCCTCTCCCA/C/A.GTGGGGAGAGACC	
		A			TGTGATTTGCCAAGTCCCTGGACCTGGACCACTACTGGCTTATGGTTGGGGTGGTAGGCAGG	
					TGAGCGTAAGTGGGAGGAAATGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGCCAG	
					ACCTAGGTCTCTCTAGAGGAAACAGGGAGACCTGGGTCTCTGTGGAT	
50	C	G	---		CAAGCGTACCTCCAAACATAAATTGATTCTGAGTATCTGGAGACTTACACTCAAGCAATCTCTGAGG	
		CGTACCTCCAA	GCTTGAGTGT		AATACTGAGGAGGGCTGGCTACTGTCTCTGCACTCTGCTGCTTTG	
4	29	A	AGTCTGCAGA		CACACTGTCTGTTTCAAGTCTGAGGTCCTGGCAGGTCAGGTCGGGTAGGCGGGGTAGCGGGTTCACA	
		ACATAATTGA			GGGCCAGCCCTGGCAGGGTCTGGCCCCCAGGTAGGCGGAGAGAGTCCCTCCCTCAG/GTTAACT	
		AGTTT			GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACCATCTCTGAAGCAGCTTGACCTCCAGT	
					TTGCACAGGGATTGTCTGAGGGCTGAGGGCTGTCCCAACCCCGCCC	
7	128	G	---		GAGGAAATGTGACTTCACCTTTGGTGCTCAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA	
		GAATGTGAC	CAGGTAGAAT		GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAA	
		TTCACTTTGGT	TTCTGTCCATT		AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTGTAGTAGGTCGTGATTAAAGTCTTAAAT	
		TTG	G		TGTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT	
					AATTCAGCAGTGTATCCACCAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG	
					AAGGTGAATATCGTTTTTGTAAACTGAATAGAAATGTATAGCGATGA	
13e	266	T	---		AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTGTAGTAGGTCGTGATTAAAGTCTTAAAT	
					TGTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT	
					AATTCAGCAGTGTATCCACCAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG	
113c	256	CT	---		AAGGTGAATATCGTTTTTGTAAACTGAATAGAAATGTATAGCGATGA	

68	G A ...	GCTAACACITTT TTAAACCGT	...	CATTTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTTCAGTATTCCTGGCCAGAGGGCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCCTGTGTGCTTCCTCTCTTATGACTGTGTCCC
142	A G CTC	GTATATTACA ATGATCACCG	...	COCCACAGAAC TATTGTAAAC AA	TTCTGAAAATATAACCCAGCATTGAGCTATTTAAACTGTAAATTTTAACTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAACACATTAAATGCTAACACTTTTTTAAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAATAAATGTGAAATGGT
70	G A ACTGA	GTATATTACA ATGATCACCG	...	COCCACAGAAC TATTGTAAAC AA	TCACGTTGGTGCTCTCAGATTCTGAGGAAATGCTTTGTATTTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGIGGGGCTGTTTTTTTGT
3b	314 C A		TTACAGAAACTTGCCCTGTGCCTGTGTCCCTCCATGCTAGGGCGGAGGGGCTTTTCTTCTCTTTC TACCTACCCCTTTTCTTGGCCAGGGGCTGCTATCTCTACCTTTCTTGTCCCTGGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCTCCCT
3	96 G C		TTACAGAAACTTGCCCTGTGCCTGTGTCCCTCCATGCTAGGGCGGAGGGGCTTTTCTTCTTTC TACCTACCCCTTTTCTTGGCCAGGGG[G/C]CTCTGATCTACCTTTCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTGATGCCAAATTAGCATTTAGTATTTTGA CAAAGCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCT
4	182 T A		CCCAGATGTCCTACACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACITTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATGTT[A/C]AGAAACACACAAGGCTT GAT
3	78 C T OCTCTGCCA	CCAACAACAT OCTCTGCCA	...	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTTCTCTGCTTCTCTCTCATCATCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACGTAAGTTTCATTGGGCAAA
6b	104 T A	CTATATGTGAGAGGGCGTGATCTGATGGAAGTTGGGCTGGATGATCTCCAAAGCTGTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTGAGTAATTCATCCTT
7	75 A G	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTACATTTTGTATTAT GCTCTTA[G/T]GATTACAGACTGATGCCAGACAACCTTGGGAAGA
10	79 T C TGG	CTTTAGAAAA TCTGCTTTAAC	...	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT[C/J]ATTCCTCTAATTGTTTCCCTAGGAAATGACTGTCCCAAG
23	107 T C GTTCC	TTGCTGGGCTGT	...	GGTCCAGAAGA GCGG	TGCTCCCTGTCCCATCTGAGTGACGGACCCAGCCACCCCTTTGAGGAGGTGGGTGAAGTCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTTCCTCJCGGGCTCTTCTGGAACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTTGGGTCTTGGGAGGGTGGGTGAATAAAGGCATACTGTCT

4	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGAGGGGAAAGAGCAGAGATTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTCATTGGTCATTCGAAGAGAGAGAGGAAAGAAAAA IT/AJACAACTTTCATCTTCTTTCGACGTTTCATAAACATCTACATA TCCTGCAAGAAGTTCCTCAAGCCTTTTGGATTTTGGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTTCTCTAAATTTTAAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA GTGCCACTACATGTTATAGAAACCATCATCTTGTCCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGCCCATTAAGGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTTAAATACATGCTGAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAT/AJTTTCAGAAC TACACAATGAATGCTTTTATTCGGTATGCATCCACATTCAGCATTTAGTGGTCTCTGAACAGCAAG TGGAAAGCAGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG GTTCTTCTTAAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCACCAAGGCGCATGCA CCGGATTCAGGTTCTTTTGTCCAGTTGTCCAGATTCCTCAAACTAGACCCCA AACAGTACACCAACACATGACAACTCGCCAGGAGGCTTGTCTCCCTCCCTCCCTTTCGCTCC ATGTGCTTAGTCAGCAAGGTGGGGAGGCACCGATGTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA[G/C]GGAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTGCTTTCAGTAACCTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAACAGCAGCTTTTGTGTTG/TTGGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGAGGAAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAAA GAATATTTGGGGAGAACCTGGAACCTGGCCACGAGGACATCCCAATATCCCTCTCTCTCAGGG CTACCCCGACATCTCTCAGCCAAATGAAGGCTCTGAA GGGTGAGACGGGTTTATTTGTCACATTTACAGCGCTCACAGGCTCTGGGCTGGCAGCGGCTGCTC CTGTGGTGGGCTGCTCTACAAGGGGCTTCACTTTCTTCCACCACTATGTACAGTCAAGTCTCCAA GGTATGGGCTACAGTGTGATCAGTGTGCTGTACACACATTTTACATAAATACACACGACTC ATACATGAAAAIT/AJAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA AACTGTTTACAAAAATAGGCTTTCAAACCTTCACTAGTAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCAGTCTAGGAGAGAACAGCAC AGAAATAAAGGATACGTGCACAAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCACTTCTCTACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG
5	118	A C			
3	242	T A			
0	165	G A			
5	148	G C			
21	41	G T			
35	215	T A			
20	202	G A			

3	184	GA	---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTGCCCATGGTGGTTAAACCTAGATGAGGGAGCTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGCTTGTGGTTCCAAGGCTGAGAGCTGGACCAACG/AJCACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAAGCGCATGTTCTCAAGTGGCCCGTGAGCAG
3	204	GA	---	---	ATGTCAGAAGAGACAGACAGACAGAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA/GA/JGCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
3b	201	GT	---	---	GATGATTCTGAAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAAGAAAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGTGGT TTATTAAATTTTCAATTCATCTGACAGCCCTTCTTATAAGGTACATCCTTGCCCTCTTCTGAGGC/G TCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
3a	85	T C	---	---	GATGATTCTGAAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAAGAAAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAAATTTTCAATTCATCTGACAGCCCTTCTTATAAGGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
1	149	GA	---	---	TTCAAGTGATAAGGACAGGCTAGAACAGCGTTCCCAACCCCTGGACCAATGACAGTTTGGACCAAA TAACCTTTTGTTCAGGGGACTGTCTACACATTTGGGATTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA/GA/JCACAACACCCCTCCCCAACAAATCATGACAATGAAAATGCTTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACTGGTT
5	110	GA	---	---	AATGATCATTTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTACATATGGTTCTTCCAGGAATCG/GA/JCAATGCTAATCTATTGCTTAA TTCCTTATCAAGAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACATTGAATGCA
3	199	T G	---	---	ACCAACCCGTTGGCAAGGCTCCCCAAGACTACCAACCCCACTTTGGTGCTTACCTATGCCGGGTG GGATTGAAGAAAATAACCAATAAATAATGCTACAAATTTTCCAGTAGTTACCAGGCACCAAGCCTAT TGAAGAAATCATAAATGTAAACCTACAATGTATTGCTCTCTGGCTGGTGCCAGGCATAGAGTT/G JGGCTACAACCCATTTTATCATTTGAACCCCTCAGAACCATCCAGTTGGGGCT
1b	157	GA	---	---	TGGTATTTTCTCTTCTTAAATGTTATGATTAAATAGTGTCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCCTAG GGAAAAGAAAGAGAGCCTGGGA/GA/JAGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

1a	48	A G ---	---	TGGTATTTTCCCTTTCTAAATGTTATGATTAAATAGTGTCTTTGTJAGJGAAATTTGAAAAATGT AAATCAGAGAACAGAGAAAGAAATAAGATATAGTTGAAACCCTCTAACAAATTTTAGATTTTAAAGGCC TAGGMAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAGCACAACAGAAAAAAGAGTGTGT GGCTAAGGGAAGCCAAGGAAAGTTAAGT
5	61	C A ---	---	TTCTATTTAAATCCTGTGCCCATTCGAAGACTGCATTAGTGTGCATGAGCCTTAGTTTCJAJTAA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGTGAGTTATTTAACTT
1	153	C T ---	---	TATTACTAGGTTCTATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCCTAACGCTCCTCACTTCCCTTCGAACCCAGCCCTCAGACATGACACTTAGGCTGCACATTCCTG TGGCAGGACTGTGTCTTCJGTTCCTGTTGGTCCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGTGCA
6	221	G A ---	---	AGAAGACAGGAGGACTGGGATCAAGGACTGATAAAGCTGAGGCTTTAATGGTCCCTTGTCTTAAC GCTTTGGTATACCTTCTCTTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGAGTTTTCAGATGTGACTTCTACATCTCGAAACTAGATGAGTTAGGCTCTCTTCACT CAATTGAAAATCTAGAAJGJAJAAACACCTAATTTGGCTCATCTTGGATCA
0	49	C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAAAGTATCTACTCTCTTACJCTAAGTGTACTTTGCA TATATTTATGGGATGATTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCT TTGTCAGGAGTTCTTATTTGGCCTCTTTCTAAACCTTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
5	31	A C ---	---	GAAACCTCGTTGGCTCAAGGAAACTGTAGJACJAAATCTTTTTTTTATTTTGTCTTAACTC AAAGAGTGGAGTTTGACCTTGATGGCAGCCTGCTCTTTGTTTGGTGAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTTAGAGCAAGGTGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAATGGAAGAAAGGTTAATGGA
12	41	A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAAATACJAGJAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTATGCTGATGAGGGCATGTACAGCCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGTGCTTGGCCAGTCCCATAGTAGGTTGCCATAAAATAAG AGTGACTAACTGAGGTAGATCAGAGAAAGAAATTTCA
52	179	C T ---	---	GATCTTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCAATTTGGAAGGAACGAGCCCTA ATTATAGAAACAGACTTACAAAGGACCAAGTTAAAGGTCTCGACACAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTCAJCTJCTGTGACAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

1	167	A G ---	---	TGGTGAAGGCTGTAAAGGCTGAAGAATAGTCTCTGCTCTGGTCTTTCGTTGGAATGGATGAGTCTCT TTTACAAAATTTTCTCTTGCCTGGGTGTTATGTTTGAATCAIGGAGTTGGAAGACTTAGATTCA ATTTGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
1	198	G A ---	---	GGTTTCATTTAACAGCCTTCCCACTGGGCTCAGATTGACGGAGATGTAATAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTATACACCTACAAAACACACATTAAACTCTCTCCCACTCTA CCGCGCAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCTCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
3	184	C A ---	---	TTTATCTTTCCAAACCATTGTGTTTTCTTCACATACTTTACGTAATTTTAAATCATGTCAATTAATTA TGCACCTTACTTGTGGTACCAGACATTGCTTCCAAATTTGTAATTCCTTAACAACAGCAAGCATAACT GATGTGCCATCTTTGTATTCCTAAA[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCCCTGTTCACCTCCCTGTATTTCCCTATTCAGCAATTCATGATTA
2	72	A G ---	---	AAAAAACAACTTCATTTGACATTCTAAGAAGATAAGAAAACAAACGATCCACTGTGTGTTGCTT GATTTA/GGGAGATAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTTCAGGAAGAAAAGCCAAATCCAATGCTAAGTTGCTAAGAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATATAGCA
5	111	C A ---	---	TGAAGGACCAGTTTGAATGCCTACCAAGGTAAAGTAATCGGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGTGC[C/A]AAAAATTGTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTTAGTAAGTAGCTAATGTTTAGATA TGATTTGAATTTGTTGCTGTGTTCTGGTG
8	177	A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTATGTAAGGTGGGGCAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG/A/GTCTCTCCAAATTCAGGGGCTCCC GTGGGATGTTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
1	34	T G ---	---	GGGATTCATGTGTCTCTCATCCAAATAGCACT/GCATGACCTCAGCCCCACTCTTTCTTCCC TATGTTCCAGAGACAGAATAGACTGGCCCCCTTCTCTAGGGGATCACAATATTTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCTTCTAGTTGA
7b	88	T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGGCTGCTTTCGTTAACTGTGTATGIACATA TATATATTTTAAATTTGATTT/GAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTGTTGTTGGGTATCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAAGTATATAATTTTTTATGTTTGTCTCTGA

a	44	T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTATGTAC ATATATATATTTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTTTGTTGTTGGTATCCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTTGTTCTGA
i	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCAITTTGTCTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAATTAATTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAAACATTTT/CJAG TTTGCAATAGAACTAATACTGGTGAATAATTTACCTAAACCTGGTTAT
j	57	G A ---	---	AGCCAGCTGGACTGATGGATGTCACCCCTTTGCTCCCTGCTCTTTCTGCCCTGGG(GA)CTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTGGCTTGAAGCT GAGAAGGCACAGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
r	69	G C ---	---	CTCTCTCTCATCCCATCACCCCTAAATAGGTCAAGTGAGGAGGCTGGGAAGAGGTGGAGGAGG G/GC/JAGAAGTGAAGGAAGATAGGAAGGATATACCTCTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCTATCACTGTAGAGGCTAAATTTATATCTATAAATATATTAATA AGCAAGTCAAACTTGGATGATCAAGGTAAATTTATGTCAAAAGTTTAAAT
j	242	T C ---	---	GAAGGAGCTGGATCACTTCCGCAGTCTTGGCAGCGCTTGTGTGGAACACAGAGACTCCTCCT CAGGGCCCTGGCAGTCACTCACTTCTATCTGTATGATGTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATATGTAACCTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACTTT
3	101	T G ---	---	CTCCCTCCTATGTCTCAGCAGCAGCTTGGGCGCACACTGTTCACTCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAATTAATAATACGTACATTTTCGAGGTAATGGTA
3	131	T A ---	---	TTTTGAGTCAAGAGACTTAAGGGCCCAATGAATTAATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC(T/A) ACTGAATGAAGAAGTATTTGGTAACCGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAACAAAGTTTCAGAGTATATTGTTGAA
4	99	T C ---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGCGCTTGTCTTTGGTTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGT/CJAGCCCCAAAGTACAGCCTGGACCAACCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

3	101 A G	TTTCTAGGCTGTACAGTCTGATGATGATTTTTTTTATAAATATTTTCACTCTTGTGAATTTGGATCTT TTTACTTTTGAAGCATATATTTAGAATATGIGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGAGGTTTCAATTTGGAATAGTTTAAAGTCAAGGAGGCTAAACTGGTCAAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
6	137 G T	GGCCAGGAGATTAGCAACAAGGATTCATCTGTACTTCTACTTGGCCCTTTTATCTTCCCTCTTGCCC CAGTCCCTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGGCAGTGT [G/7]CTACTCCTCAGGTCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAAAATGTCATCAG
	252 C T	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAATAGATTCAATTGGATCCCCAAAATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTTGCCAGAAATTCAGGTGAGTGGATGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTTTGTCTGTATTTGGCATTCCT[C/
	218 C T	GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTGTCTGGCAOC CATGATGGAACCTCTTGCCATGTTTTAGTACCCCTGGACCAAGTAGTCAATCCATCTGACTTTTAAAA TTCTAAACAGCCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C/7]TTTAAACAAGCATAGATAATCTGAACAAC
ic	146 T C	TTATGTTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGT[C/CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
5b	146 T C	TTATGTTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGT[C/CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
4	165 G C	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTTCAACCTGTTTGCAGCCCAAGTNCCTTCCAAAGAGGCTCAGACTACCTCTCCATCTCCCCCT CTCCCCACAACACACAATAACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTTAGTTTCTCAAAATGGGAATGG
6b	25 A G	AGCTTTTGAATCCAAAACCCACATG/CJCTTGAATCTCTTATCTCTCTCTTGTGTAACTATATCC CTGAGGCAAGAAATACAGAACACCCCTGTTGGCTGCTGAACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTCTGCTATCCCTGATGACTGGGCAAA

25	A G	AGCTTTTGAATCCAAAAACCATATGAGCTTGACTCTCTTATCCTCCTCTGTTGTAACATCTATCCCTGAGGCGAGAAATACAGAACACCCCTGGCTGGCTGAACGGAGGATGGGGGGGAGACATCGGTCAATGTATCAAAGCATCTCTGCGCTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGCTCTGGCAAGGGCTTGCTTATCCTCCTTGCTATCCCTGATGACTGGGCAAA
59	GA	TTTCCCAATCCACAGGTAAACTAATATATGGATGTATAGAATTTAGAACTACTCCGAGJTTTTTTCCCTGGGAAATATTCACAAAACATTTGGTGCTGCAATCAGGTTAAAGACATAGTGTGCCATTTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCATGCTGTGAGACTTTATGTTATCATTTATTAGAGCCAGGCTTGCTCTGTACCCAGCTTTCAGTGAGT
106	T C	CTCTCACTCCCAACACTATATGCTTACTTAATGGTTACAGATTAGCCCAAGGAAGCCCTGTCTCAATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAAATAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCATGCTTTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
106	T C	CTCTCACTCCCAACACTATATGCTTACTTAATGGTTACAGATTAGCCCAAGGAAGCCCTGTCTCAATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAAATAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCATGCTTTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
103	T C	CTCTCACTCCCAACACTATATGCTTACTTAATGGTTACAGATTAGCCCAAGGAAGCCCTGTCTCAATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAAATAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCATGCTTTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
141	A G	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGGATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATGAGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATTAACTTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAAAT
141	A G	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGGATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATGAGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATTAACTTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAAAT
136	A G	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGGATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATGAGJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATTAACTTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTAAAT

				TTCAAAATTAACACCATGGGTATATTATTAATTTINGCTCTATCCATAGTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCAATTTCTGCTGACCCCTCCCTCCTCACCCCTACTGGCTCTGACTTCTCTTCTGGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTCTGCTGGCTCAATAC
66	GC	---		TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGGTGGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
b	156	AG	---	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGGTGGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
	156	AG	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
b	119	GA	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
	113	AG	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJGJTTGTGTTTGGC CAATAATATCTCCCGAGGACGTCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCTCCCGCACAAAGCACACATTAGAAACTTA
	119	GA	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACGTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA
b	123	CG	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACGTATGGCCTGAATTTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA
	123	CG	---	TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCJGTATTTGTACATAA

198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTGGTNCCTGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGAAAGGTATCCTAGTCCATCCCTTTATAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
205	G A ---	---	CAC TTC AAGGGCTCTGGGGANGAGCGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAITTTAATCAGGAGGAAGAAATCTTCCGAG
205	G A ---	---	CAC TTC AAGGGCTCTGGGGANGAGCGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCTCACGCTGGCCCCCAAGAAAGTCTTGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAITTTAATCAGGAGGAAGAAATCTTCCGAG
90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
167	C T ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[CT]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
155	G A ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
181	T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATATGATGTCCTAGGTACATTTGTTTTTATTTGTTCTG CGAATTTGTTATACCTTTGGGAGAAATGCTCAACTATAAATATGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GGCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATGCTCTGGCTTCATTTTGTAATNTG

17b	204	GA	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTTCACAGGTTTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATCCAGCCACCGCAAACCTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGAGGCAATTACCATAAATCACCTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATAGGCAGA
18b	147	CT	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATCGCCAGGTGGC TAAGTGTGGGGC/GT/CTGGGGTCAGGCTGCGCTGGGTACATCCTGGCTCCAAACTGCTTGTCTATG GCT
18a	124	CG	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCGCTGGGTACATCCTGGCTCCAAACTGCTTGTCTATG GCT
14	124	TC	---	---	AAGTTTACAGAAAATAACAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGNCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN/T/CJGNCA AAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GCG
15d	202	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05c	46	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
15b	153	TC	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
05	202	CT	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

				TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTGTTGNNNNNTNG GGCTGGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTACCTAAGGGGAGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTGAGTGC
b 248 A G ---			---	TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTGTTGNNNNNTNG GGCTGGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTACCTAAGGGGAGAGAGTGGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTGAGTGC
240 A G ---			---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACITTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGGTGGGGAGCAGTGGGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTTAAATGTAICTTTNCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
b 118 T C ---			---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCTCTCACITTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGGTGGGGAGCAGTGGGTAGGCAAT/CJGTGAGATTGCTTTT CCTACCCCTCTTAAATGTAICTTTNCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
118 T C ---			---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTTCCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
3b 169 T C ---			---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCTTTCCTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
5 165 C T ---			---	CTACGATAATTAGGTTTGGCAGTGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/CJGAAAGTTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG
7b 162 T C ---			---	CTACGATAATTAGGTTTGGCAGTGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG
7 175 C G ---			---	CTTGNCGTGAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG

41b	136	GA	---	TATCAGCATGATTGGCTGTGGACACAAAGTCAATTGTACTTTTGNIGNNNCTCTTTCTNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTGTNAAITATACCCAAGC G/AJGGATTGTGATGGATCTGTTTATTTTCTCTGTCTTGAACAGCAGAGTCGTCTCTGNGAGTNG GTTTCAGGATTGTCTGTCTGTTCCCGAGCCCACTTGCACTTAGCAAGTGT
49e	192	GC	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
149d	264	CA	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349c	192	GC	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349b	264	CA	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
349	264	CA	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
1403b	57	CT	---	TGGTATTGGAAATGGGTTTCAGACTCCGGTTCTGGCTTCGACCTTGGTAAGTTGCTTCCGAA GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG AAAGTTTACATCAACATAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
1403	58	T C	---	TGGTATTGGAAATGGGTTTCAGACTCCGGTTCTGGCTTCGACCTTGGTAAGTTGCTTCCGAA TGGCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT

c	31 C T ---	---	CAGCCCGGAAGAGATCACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGAGCCACGGG GGTGACAGCATGCTGCGCATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTGCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGTATTTAATGTTGCTTTGTAGAAAAGTGGC
b	31 C T ---	---	CAGCCCGGAAGAGATCACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGAGCCACGGG GGTGACAGCATGCTGCGCATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTGCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGTATTTAATGTTGCTTTGTAGAAAAGTGGC
a	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTTAGGGGCATGTATCTGTAATCTT TTTATTTCTCCAAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTGCTCTCCGTGGTACCTTCTCCACCACATCAGCTGTTTT
2b	122 T C ---	---	TGCCTTACTCTTTGTTCAATCCACCATTAATTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATCAAGGAGTNTCCCTGGTCAAGCCCTT/CJATTGAGTCT CTGCCACATGCTAGTAAGTGTGATGGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
2	114 C T ---	---	TGCCTTACTCTTTGTTCAATCCACCATTAATTTGTAAATGGAACTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATCAAGGAGTNTCCCTGGTCAAGCCCTT/CJATTGAGTCT CTGCCACATGCTAGTAAGTGTGATGGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
0	97 A G ---	---	GCGAAATTAATGACTCCAAAGGTAGTAATCCTTTCCCCCAAAAAGGTTTTAAAATCTGTGTGGA CATAATGTTGAAATTCAGTTACCTTGGAG/JTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
10	31 A G ---	---	GGTACACAAAAGAAATGCTTCTGGAAATCTAC/JGTAGCGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCCACCATGAAGCTGGGCAAGAACAAATCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCAGTGTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAAATATCAATAAAAT
33c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCAATAATAATTTTTCAGGCAGAA CCATTATGAT/JAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTACATATCCTG GGTGCTAATTTCAATAATATCTACTAAAGCATGACTTCTAGAAAATTAATTTACTTCTGTGCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA

103b	77 A G	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGJAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATCTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
137b	112 C T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAGTCTGGGGAACGTTTGTAGCTTCTGCTGGCT
137	112 C T	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAGTCTGGGGAACGTTTGTAGCTTCTGCTGGCT
340b	79 G T	TCACCTAGGGAGGTGCTAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/JGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCTTAAGAGCCATGAAGAAATTAAGACT ATCGCA
840	79 G T	TCACCTAGGGAGGTGCTAAATGTAGCTTCATTAAAGACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/JGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTTACTAAAAGTTCTTAAGAGCCATGAAGAAATTAAGACT ATCGCA
879b	110 C T	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/JG/JGTCGTCNAAATAAATCCCCAAA AAGTGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAG/AAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
879	110 C T	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTCTTTTCATTAAGTACTCCCCCG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/JG/JGTCGTCNAAATAAATCCCCAAA AAGTGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAGAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
900b	119 C T	TGTTCTCTGGTCCAGGACCGGCTAAGTCTGTCTGCATAATGGAATAATCAACTGGACAAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/JGCTCTGAGAGGT AAAGTCCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGAGAAACCACTTTCTTTTGTCTC

10	119 C T	---	---	---	TGTTCTCTGGTCCAGGCCACCGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCCNCG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACCTGCCATGAGAAACACATTTCTTGTCTCC
13c	165 C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGTAAACATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCCCTCTCTCTGAANCTGGTCCACGCTGGAGATAGTGA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGCTGGAGTAT
13b	165 C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGTAAACATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCCCTCTCTCTGAANCTGGTCCACGCTGGAGATAGTGA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGCTGGAGTAT
43	164 C T	---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGTAAACATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAGACCAGCCCTCTCTCTGAANCTGGTCCACGCTGGAGATAGTGA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGCTGGAGTAT
60c	270 A T	---	---	---	CCAGGTAGGGTGAAAGGAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGGTCTGCTGGGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
160b	270 A T	---	---	---	CCAGGTAGGGTGAAAGGAAGGAGGCAATTGCTGTTGGAGTGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGGTCTGCTGGGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACCTTAAAATGCACCTCCCAACTTT
177	203 T C	---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGATCA TTCTGGGCATTTCTCATAGAGTNTGTTTTTAGTCTGTAATACTGTTGCCCTAGGAAGTTGTT TTTCTACTGGCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C/TAAACAACTGAGCTGGCTGAGGCTGTTGG
112	102 T C	---	---	---	AAATTCAGAGGCAAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCGCACAAACTAGCTAAAATCTTCTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

3	127	C T	---	---	CTTTAGAGGTGGTCATTTCGGTTCCTCTGGAAAGTGATTGCTGTTTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTAGCTTCTGAGCCCTGGTTACTGCAATCC
32c	166	G A	---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAC/GATGTGGGACCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTTAGGCTCACCTTCTCTGTAATTGCTTCTGTTTTCAAGGG
32b	219	C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCTCTGGCAAGCCAGCCCTGCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTGTCTCAACCTCCGACTTTCACAGA TCAATGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTCAAGGG
32	219	C G	---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATAACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/C/TTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54b	188	C T	---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATAACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/C/TTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
54	183	T C	---	---	TGGGATTAACAAACCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAAGACAGATAAAATAGCTCTTAAATGCACCTTCCCGTTCACAAGGTGTTTCCGTC/TT/C/TTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGTAAAGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG
73d	129	T C	---	---	TGGGATTAACAAACCTGTTTCTTCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAAGACAGATAAAATAGCTCTTAAATGCACCTTCCCGTTCACAAGGTGTTTCCGTC/TTTGTATAT CATCTGATCTTCCCAACAGGGCTTATTTT/C/TTGCTAGGTAGGTAAAGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG
73c	165	A C	---	---	

3d	129	T C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCCTGCTTTC/JTGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
3c	165	A C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCCTGCTTTC/JTGA CATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
3b	165	A C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCCTGCTTTC/JTGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
3a	129	T C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCCTGCTTTC/JTGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
38b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTTC[J/G]JCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGGCTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAATGAATATCGATATAC
68	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTTC[J/G]JCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCACTCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGGCTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAATGAATATCGATATAC
70b	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTGGGAAATTAGAGCAAGGAATTGTATAATCTTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
370	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTGGGAAATTAGAGCAAGGAATTGTATAATCTTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT

14c	49 T A ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACAAGGCATAAAAAAT/A/CAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
34b	41 A G ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACAAGGC/A/GTAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
34a	38 G T ---	---	TTAGCACATATCTGTTGGGACCTAACTGAGACA/A/GTGCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCAATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
71b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTCTTTCAAACAATTTGTAACTCCTCTCTCTTAATAAACCTTAAC ATTCTTTTGTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT
71	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTCTTTCAAACAATTTGTAACTCCTCTCTCTTAATAAACCTTAAC ATTCTTTTGTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT
195d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTT/A /TAAATCTTTCTTCTGGT/GT/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
395c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTT/A AATCTTTCTTCTGGT/GT/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGT
395d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTT/A /TAAATCTTTCTTCTGGT/GT/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
35c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95b	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
95a	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
47	85	C T	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAG ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTGTTTCTTACTCTATCTCTGAGACTTCTTCTCT GAATGAATACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGGCAAGG
34b	68	T C	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATCTTTATGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAAGCAAGAACAAACAGAAAGCCCTGTGTTGCAATCTGGCTCTTATAAATACTTCTGTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATATCATCTTAAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
34	68	T C	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATCTTTATGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAAGCAAGAACAAACAGAAAGCCCTGTGTTGCAATCTGGCTCTTATAAATACTTCTGTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATATCATCTTAAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

92b	106	G A ---	---	GT TTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATOC TCCCTGTCCCGTCCCAAGCCTAIGTTACTGGTATGCTG[A]TGGTATGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGTAATTAATTAAGTAAATATATTINCCATGA GACACAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
92	106	G A ---	---	GT TTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATOC TCCCTGTCCCGTCCCAAGCCTAIGTTACTGGTATGCTG[A]TGGTATGGATGGGATGGATTA GCCATGAATATTTTCCATTGTTTCATTAATGTAATTAATTAAGTAAATATATTINCCATGA GACACAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
155	19	G C ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACATTTCCCAAGCATTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAAGTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
108	194	G A ---	---	CCATGAAGATGAGTTCCTCCCTCCCTGGGTACGCTAAGAAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGATGGCTGGATTCTCCGCTCTAAGACACACCTTTATGCTTTNAAAGCTTT CTGGAAATGGGATGAATCTNACATTTCAATGTCACCTTCGTTGGGATCATTCTCC[G/A]TGCCCC ATCTCTGNAGAAAGCCACTGGGAAAGTCGAAAGAGTGACTTCAATCAGG
305b	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANNGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
305	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANNGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
364b	177	C T ---	---	GCTAGTAGGTTCCACCTAAATGGTCCAAAGTCAGGAGAGTCACCTAAATGTTTGAGAAATAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAAGCTTAACATGCATGCTGTT[C/T]AACAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACA
364	177	C T ---	---	GCTAGTAGGTTCCACCTAAATGGTCCAAAGTCAGGAGAGTCACCTAAATGTTTGAGAAATAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAAGCTTAACATGCATGCTGTT[C/T]AACAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACA

19	64	A	G	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCTCTAGTATTCCTTTAGTGGAAAGATTCA[G/G] AGACCAGTTTGGCTTCACTTAGTAGGGCCAAATGATAGACTTTTAGTGCTACCAAGGTTACCTGC ACAGCCACATCATGTGCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCTGCCCTTGCTC TTCCCTGTTTTACCATATTAAATGATGACATGCAACCTCAGAGCCTTTA
24b	133	G	C	---	ACAGTACACATGCCCCCATTTATGAAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGCGAGTGCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATG /CJAGAAAAAATGATAGTCAAGTTGAGACACTATTTAAAAATTGTAACTTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTTATGTTTNAATTACTGCCAATCAGAGCCAAG
74	133	G	C	---	ACAGTACACATGCCCCCATTTATGAAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGCGAGTGCTTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATG /CJAGAAAAAATGATAGTCAAGTTGAGACACTATTTAAAAATTGTAACTTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTTATGTTTNAATTACTGCCAATCAGAGCCAAG
82	137	G	A	---	CAATATAGACCAAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTT ATTGGCTCTTCTTTCTCTCTCTTTTAAATGCTCTCTCCAACACCAATTCACITTTATCTTTCAA T[G/A]AGCATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTTCAAACAAGTATACATTAA GCCTGCAAAAGTGCTTATATGCTAT
54b	194	G	A	---	GGTATGTTGAGGTGAGTCACTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTGGA CAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAATGGCCTGTCCCACCTCCACAGAAATGGTTTAAACAGAGTCAGAGCCA
54	194	G	A	---	GGTATGTTGAGGTGAGTCACTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTGGA CAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAATGGCCTGTCCCACCTCCACAGAAATGGTTTAAACAGAGTCAGAGCCA
39	210	G	A	---	AGCCAGCCACATGTTGAGTCTGCTCATCTTCCATCTCTATTTCTCTCTACTGCTTACCTT CCATTAAACAAGAACTTGTGATTACATTGTAIGTTTGGTTACACTACAGAAATCCAAGATGACCTC CCCTCTCAAGGTCAACTAATTAAACACCTTAATCTATTTGCAATCTTTGTGATTACCAATACATATT CATGG[G/A]TTCTGGGATAAGGGTAGACATTTTATGGGAGGCATTA
10b	130	T	C	---	GAAAAATGATGTTTTGATTTCCCTTCCATCTTCCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCCTTCCCTGCTTTATTTTGGCTT[C/JA]CA GTTTAGGTAAATAAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTTGGGGGTTTTTCTGGGAAGA

					GAAAAATGATGTTTTGATTTCCCTTCCATCTTCAGATTATTGGAGTGTTCATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTGTCTATAATTAAACCTTCTCTTCTGCTTTATTTTGGCTTC/CJACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGTTCTCTGGGAAGA
0	130	T C ---		---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
9b	168	GA ---		---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
9	168	GA ---		---	CAAGTCAGATTTTGATTTCAGGATAACAAATTTGAAAAATAGAAAAGTG[G]TTTAAACTATTT CAATAAACATAAAGAAACATGATGAAATCTTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3b	51	T G ---		---	CAAGTCAGATTTTGATTTCAGGATAACAAATTTGAAAAATAGAAAAGTG[G]TTTAAACTATTT CAATAAACATAAAGAAACATGATGAAATCTTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
3	51	T G ---		---	TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATAC GTGCTGT[G/C]CCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAGT AGGACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
9b	145	G C ---		---	TTGTACATGTTCAATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATAC TIC]GTGCTGTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTGCTTGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
9a	137	T C ---		---	TAACACACTTTTCATTTGGTTTCTTACTGCAGTTAAAGGACCATCCATTATATACAATTCCTC AGTTCTATGCTTTAGAGTNCATATATAGGACTACTGTAAATTTTCAGAGGGAATTAAGTCTGGAGTA GGGGAATGAGTTAAATATCTACCATGCCAATTCAGAGGACTGTGGTTAA[G/A]ATGTCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG
82	188	GA ---		---	

					AGAGACGTTGAATGGGACATCTTTCTATTTGATTTTGAATTTTAAACATTTGATAAGAAATGATGAAA GTTTGCACATCCAGATTTATCTTTATAGCAGCAGAGCTGCGCAATAATAACAGCACACTGACT TTTCCATGGTAAAGAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGAAATGATGACCTTTGAAATTTTGAATTTATGG
10	93	T	---	---	GAAAATCCATTGAAGTTTTGACCTTGAACCTGATCTCATTAATACTTTTNCCTGAGTGTGTTATTT CATTTTGGACACAGACAGCAAAATTTCCAGTTAAATTAATTTCTC/TAAAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTTATCTCTAGATATTCTTCAGAAATCTAGGATGGAAG AA
11	118	C	T	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
71b	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
71	151	A	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTAACTTACATGATJNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89b	156	G	A	---	AATCGAAACATTGATTTTTTTGTAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGATGAACCTGGAGGAAGAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTAACTTACATGATJNGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
89	156	G	A	---	GATGACAAATATTGTGATTTGGCATTTTAAJGJGTACCATCCATTTCTCTGGCTTTCTGTGTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGTATTGCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAGAAACATAAATCAAAATTG TATTATCTCTATGCTTAAATGCTCAG
188	31	A	G	---	ACCATCAATGTATCAGCTCTAAATTTATTAGATGATTAACCTGGCTCTGTTAAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAAGATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAGGCGJGTTTTTGGAGGGGAAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTGTCCCCATAAATAAAATTTTACATGCTCT
191	145	G	C	---	

84	144	A G ---	TTGGTTGGCATTAGCCTCATAAACAATTTACAACTAATAATTGTTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGAGCAAGATTTGAACCCAGGAATCCATT CACCGGTAC/GJTGCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAAATAGGTGCTTTAATTGTTTATCAGTATGC
39	185	C T ---	TTTTCGATTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTATTTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAITCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
127	63	A ---	AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGCTGGTGAGGATGGTGGCTGAGAGA/- JGATTACTCATAAAGCATAATTAATTTTATAAATATGGAAATTTAATAGATAAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAAATGGCTCTTTGGGATGACAAATGATGAATGTTCTAAGCAGACAG
390	87	C T ---	GCCTTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTAT[C/T]GTCTGTCTCCCTCTCTGGTATGCTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATCGTGGCTCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTGAGAAATGAACTGTGAATCTATGGAAGACAAACGAAT
404b	87	G A ---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTAAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
404	87	G A ---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTAAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
545b	77	A C ---	TAGGAAAGGGATGGTGATGGCTCTGAGACATTAAATCTATTTTACCACCTACACTGCCGCCA TATCTCCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
5545	77	A C ---	TAGGAAAGGGATGGTGATGGCTCTGAGACATTAAATCTATTTTACCACCTACACTGCCGCCA TATCTCCTC/A/CJCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

					ACTCAAGTTGGGGATAAAATCAGAAGTTCTCTGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTCTTAAGGAACTACATCA GJTATACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
860b	134	A G	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTCTGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGAATTTGTTTACTTCCCTAACCAACCTCTTAAGGAACTACATCA GJTATACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
860	134	A G	---	---	GCAAACAACCTATTATACCTGATTCACACCCAGGTCTACTAACATTAAATCAACCTAACCAATAC TATATATTGCTCTGTTCTGAATTTTTCATTTAGAACTCTGATGAGATTTAGCATGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGCCTCCAGGAGTCTCAATGTGAAGTATAATTTCTACAGAG TAATTCGJATAGTAGGTACCCACAAAGTCTATATTGTATGTGAAGGAAAG
3106	208	C G	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
6109d	129	T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAA ACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT TGNAAAATTATCCCTGAAATTTTATACCA
-6109c	147	T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAA ACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT TGNAAAATTATCCCTGAAATTTTATACCA
-6109b	147	T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGCGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
-6109a	129	T C	---	---	AATGCCTATACCTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGATTCGCATATCCCAAGTGCCTTAGACAAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTTGTTAAATCAATAAATTAATCAACTTGGCATATGCAGG GMC
I-6112	96	T C	---	---	

44	103	T C	---	---	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAAGAATAATTCCTTTCTTTAGTGATT GCTTAATATAATTAATCATAAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTAGAAAGAGG AAATTGAGTGTGGGAATTAAGCAACGAGGAGACATTTTATATACTCTACAGTGGGGGAAGACTT CCTATTTCCTTCCCAAGGATGATACATTCTAC
68	124	C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTCTCTCTAGTAGGGCTTGGGTGTGGCACCGTTGGCTCAATCTCTCTCCCT GGGTCTTATTGACTTTACGGGAGCTAGAGAGCTGGACAAAACCTGCTTCTTGCAGAAAGAGTCG GGGTCCAAAGATTGTTACGATTTTATA
136b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTCAATTAACAACTAAACAGCTT ATATACTGGCAATATAATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTCAATTAACAACTAAACAGCTT ATATACTGGCAATATAATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCCCTTGGAGGACACTGACAGT
381	92	C A	---	---	TTGGATACAAAAATTCAGTTACAAATCAGTACAGTCAAAATAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAAACAACAACTTAAAGCTCAACATTTTAAACAGGCACAAAT ATCTAANGGCATATGCATTCACCATGGCTTTGAATGCTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTAGGCGAGTAGAAATGGACATTTTAGGAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGCATAATAAGAAGTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGTAGGTCGCTTC GATTGGGTGATTCACAGACAGAGGTGATGTTCTAAGATTGTATTTATTGT
449	186	C T	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCATCTGCAATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTTAATTTTCTGTGGTATTATA
449	186	C T	---	---	GAGGCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTCAGCTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCATCTGCAATCTCTGATCTTATGCTGGCTCTATTCCTATCCCTATCTCTGA TCTTATGTCAGACCTGAAGTTCCTTAATTTTCTGTGGTATTATA

63	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGA AAAAATTAAGTAGAACTCAAGAGCCAAAAGTCCCAATTTGTGTCATT TAAGAAATATTTGAATGGAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTCTCTCTC CAGTCCCATTATATGACATTCGGCATGCTG
174b	76 C T ---	---	AAGCAGTAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAGTATAAAGAGTGAGCCATACTTAGGGTACCATAA
474	76 C T ---	---	AAGCAGTAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAGTATAAAGAGTGAGCCATACTTAGGGTACCATAA
478b	175 T A ---	---	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTA CACTGCTATTTACCTCCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACAACTG
478	175 T A ---	---	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTA CACTGCTATTTACCTCCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACAACTG
3559	149 G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTAOCCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTCTTC
3564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTTACCCAGGCCACTGTCTCTATGC[G/A]CACTGGCTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTCTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTTACCCAGGCCACTGTCTCTATGC[G/A]CACTGGCTTG TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGGTCTGTGTAAG GTTCTCTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

08b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTCAGGAGCTAAGGGAGGGGATTCCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAGGAA AGC
108	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTCAGGAGCTAAGGGAGGGGATTCCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAGGAA AGC
166	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNTTCTCAAGTCCAGGCTCTTGGGTAGACCAAACTA ATACAAATGTTAGAGCACACAGAGA
370b	120 A G	---	---	AGATTACATAATTATCTAGGGGCAATGTAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC[AG]TTGTAGCCA GCATTGCCATTTCAGGGCCGAGTCAGGGTTTGTGGGCCAGAAATTTAGACAAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT AGATTACATAATTATCTAGGGGCAATGTAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC[AG]TTGTAGCCA GCATTGCCATTTCAGGGCCGAGTCAGGGTTTGTGGGCCAGAAATTTAGACAAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT TTTGAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
704c	33 T C	---	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
704b	33 T C	---	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C]TAACCTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG
3704	28 T C	---	---	TTTGAAATAAATTCATGCACCAATGTTTAACT[C]TAACCTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATTAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCAIGAAGAGTCTAGTACAAGATAGGCAGACATG

10	106 GA ---	---	COATGGACAGTTTAAITAGGAAGCTTCGACTTGTTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTTAAACACATTTTGTAGGCTGGAATGATTCCTGAGTAGTAACCTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTTACTAGTGACACAGGATGTCACCGAGTCCAGCTC ATCTCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCTTGGACAGGAAGGGTC
66b	148 GC ---	---	AAAAAAATGGTGCAATGCAATAATTTGGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAATCCAGTCCCTCTCTC
66	148 GC ---	---	AAAAAAATGGTGCAATGCAATAATTTGGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAATCCAGTCCCTCTCTC
787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAATTTTAC[G/C]TTTACTGCATAAGATATCTTCATGTACAACGTGT ATGCTTTGCTCTCTGGGAAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
793	105 CG ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATATGATAGCAAGTTTCAACACATTCA TCAACAAGGGCGTCTTCAATCAATCAGTCAACCCCG[C/G]GAGTTAGAAAGTAGATCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
3810b	37 T C ---	---	CACAATAATAAAATCACCTCCCTACCTTGAAACCTTTAT[C/G]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
3810	37 T C ---	---	CACAATAATAAAATCACCTCCCTACCTTGAAACCTTTAT[C/G]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
6817b	145 CA ---	---	GCATGATTAACCCAGTGCAGAAAATACCAAGTACATTTGGGTGAACGATGAGTAGCTGTTCTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCATCACTAATCAACAATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCTGTGTGCTCTACTNGCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAATCTTGGTTCAGGTGGCGCTGTGCAG

317	145 C A ---	---	GGATGATTAACACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAAATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C]A[AT]GTGGATACCCGTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAACTTGGTTCAGGTGCGGCCTGTGCAG
319b	221 C ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTTCTCTATATGACACCTAATATCCAG
819a	175 GT ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTTG TTGCTTAGCAACAGCAATAACTTTTGTTCTCTATATGACACCTAATAT
826b	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[AG]GAGCTTAAATAATATCAAAATGCAAAATAGATTGGTGCAGTGT TAAGCTGAATTGCAATATTGGCAACACACACTGGACTGGGTATACGTTG
3826	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAACAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTGCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[AG]GAGCTTAAATAATATCAAAATGCAAAATAGATTGGTGCAGTGT TAAGCTGAATTGCAATATTGGCAACACACACTGGACTGGGTATACGTTG
6857a	122 T C ---	---	AGTGCAAACTATTTTGAACAAAAGTAACTATGAGTCACAGCATTGAGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAGTTTGGCAACTGTTTGGGCTAATT
6865	153 G A ---	---	TTATAGAATACTTATGGGGCATACNGTAAATGAACCTGCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGCTGAAATCCTCCCTGCTCACAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAACTT[C]A[AT]AGAGCCATTCGTGCAGAGGAAGGGAAGGAGCTGTTTGT TTACCTGTAGTGAAGATATCTTTGGCTGTAGAACTGAGCTCATTA
-6909	73 C T ---	---	ATTGAAACTGGTTAGCAACAGATAAATTACAATAGAGCTGGATATAAAATGAGAGAAGATGC AGACTT[C]T[AA]AGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTATTCGAATAATAATCTGCCAGTGGCAATCAG AAACACCATTTCCACAATATTGTCATGCCCTAGTTGCTTATTTATACATATC

310b	163 G T ---	---	CACTCAAAACCCTTTATTCATTGATTTACAAACTGTACAAATATTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGCTAAATAATAATATGTGGCACAATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
915	144 A ---	---	GCCTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCTTGGGGCACTTCTTCACTTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGGGTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTCAGATTTCCCAACAAAGAACATG TATTGCTTTTGTAAATTTGAAAAAATAATCAACACAGGATAGTAAAGATAT
928b	175 T C ---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTCTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGAAAGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
3928	175 T C ---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTCTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGAAAGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
6955b	79 G A ---	---	TTTTATGAACAATTCAGATTCCTCATATCAGCAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
-6955	79 G A ---	---	TTTTATGAACAATTCAGATTCCTCATATCAGCAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
-6957	47 C G ---	---	AAACTAAAAACCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCAATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTTGAAGAAGTGGATTGAAACCACCTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTATCTAGAAAAATCATGC
1-6996c	242 G T ---	---	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCCTCTGGTCCCGCACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTCAGCACCCAGAGAGGAGAGAGCGCGGAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCC[G/T]GTGGGATC

996b	242 G T	---	---	ACTTAGTGCCTGTTAGCACACACCTCTAATGCCTGGTGGCGGCACCTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGTCCTCCCTCCCTCTGCTTCAGCACCGAGGAGGAGCGCGCAGTTCCCTG CAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTTCGCTGGTGGGATC
996	228 T G	---	---	ACTTAGTGCCTGTTACCACACCTCTAATGCCTCTGTCGGCGGCACCTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGTCCTCCCTCCCTCTGCTTCAGCACCGAGGAGGAGCGCGCAGTTCCCTG CAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTTCGCGTGGATC
7021b	112 G A	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAAATGAGCCGACTGCACCTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCAATTAATCAAAAC ACTGTTAATACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7021	108 A G	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAAATGAGCCGACTGCACCTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAAATCAATTAATCAAAAC ACTGTTAATACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
7056c	118 C T	---	---	GGCAGTAGGACACACAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCACAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCAGACGGCTAAACGTTGGTGA[CT]GGTGGGAGCCCTCT GGGCTGTGTAAGTACCTTGTGTGTTCCAGTTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTGGCATTGATA
7056b	118 C T	---	---	GGCAGTAGGACACACAGTGTGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCACAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCAGACGGCTAAACGTTGGTGA[CT]GGTGGGAGCCCTCT GGGCTGTGTAAGTACCTTGTGTGTTCCAGTTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTGGCATTGATA
7091b	153 A C	---	---	AATCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATACCTCTATAAATAGTATTCACATCACTGTG CTTAATTTAAATAGCAT[AC]TCTATCAATATCAGCCTTTTATGTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
7091	153 A C	---	---	AATCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATACCTCTATAAATAGTATTCACATCACTGTG CTTAATTTAAATAGCAT[AC]TCTATCAATATCAGCCTTTTATGTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

36	58 T C ---	---	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACGTGTCJAATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGCAGCAACATGAAAGAGCATATACATATGTTG GTGGAGAAAGGGAAGGGTTGGCTTTTAAATTTATTTCTTCATCTTTATAACAAGAAAGNNNNN NNNGTAGCTTTCTATATAIG
46c	210 A G ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGCTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCCAAGGCCCATGCCCCGCG TGGTGACAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGCCCTCTCCGATGCC AACGC[AVG]TTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
46b	210 A G ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGCTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCCAAGGCCCATGCCCCGCG TGGTGACAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGCCCTCTCCGATGCA AACGC[AVG]TTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
46	202 G A ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGCTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCCAAGGCCCATGCCCCGCG TGGTGACAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGCCCTCTCCGATGCA JCCAACGCAGTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
153	161 A T ---	---	ATATTACAACTGCTTTTAGCTGATCTCCATCTCCAAATGACTCTTTTCTTTCTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTGATTTTATCAGGAAGTATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNN[AT]AAAAAAGTTATTTAACAGTAATCTATTACTAATTTAT AGTACCTATCTTTAAAGTATAGTACATTTACATATGTAATGGTATGTT
155	156 T G ---	---	TAGAATAGATGCGGTCATATCTCTTTGGCTTCTGGTCTCCAGCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACCCAGCTGGCCCTACCCCTATAATGATCTGTCTCTAAATTAATACAC CAGTGGTTCTCTCCCTGT[GT]AAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTCTAG TCTACTCTCTGTCCCAACCTCTCTCTCTCCCACTCCCACTCCAG
169b	161 A G ---	---	AGCTCCACCAGATGCAGATTTGTTTGTCTTGTATCACTGTCACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGCTAGCCAGCCATCAAGTGTCTGAAATTCATATTTGTTTATGCAAT ACAGCAAACTTTTATTAAGTAGAT[AG]GGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAATGGAAGTGTTATATA
175b	194 C T ---	---	CTCCTAGACTAGTCTTACCTTTATTAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTCTCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAAAGGCTGGCTGAAATCAGTATAACCATC AGTTACTGGTTTCAGTTGACAAAAATATAAATGGTTTACTGCTGTCATGTCATGCTA[CT]TAGAT AATTTATTTTGATTTTGAATAAAAAACATTTGTACATCTCTGACTGCTGGG

75	194	C T ---	---	CTCCTAGACTAGTGTACCTTTAATGAACGTGTGACAGGAGCCCAAGGCAGTGTCTCTCACCA ATACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGTCAATTGTCCATGCCTA[CT]TAGAT AATTTATTTTGTATTTTGAATAAAACATTTGTACATTCCTGATACTGGG
78b	273	G A ---	---	TGATCAGGTCAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTCACTGGCTGGCTCTAGGGGAACAGACCAGTACCCCAGAAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
78	273	G A ---	---	TGATCAGGTCAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTCACTGGCTGGCTCTAGGGGAACAGACCAGTACCCCAGAAAAGCATACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
182b	116	A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCT[AC]TCTCTCCTCTATTT TACTTGAGGCTGCCAATACCAGCCCCAGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAATT
182	106	C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCC[AC]TCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATACCAGCCCCAGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAATT
191b	273	T A ---	---	ATAATTGCTGTTTCTAGCCTGGCAAGATATTTCTATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACACAGCACCATCTAAGCATTAGTGGTAGC TGATGTCAGCTTCAATGTGGATTTAAGCACTCTAGAACAAATGAAGCTTCTTGGCATATTTAAGGAG CTCCAAAATGTGTACCTATTAAATTTAAGTCAAGTCAAGTAGAGCATT
199c	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCAAAATTTGAGTTGACCCCTTCCCTGTGGCCTTAGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[AC]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTGAAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
199b	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCAAAATTTGAGTTGACCCCTTCCCTGTGGCCTTAGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT[AC]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTGAAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA

WI-7216c	237 T C ---	---	---	TGACACTAAGACTCTAATTCAAGCGAATGTTGGAAACACCATGACCTCCTCTGTGTGCTCTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTTCCTTGTAATCATT
WI-7216b	237 T C ---	---	---	TGACACTAAGACTCTAATTCAAGCGAATGTTGGAAACACCATGACCTCCTCTGTGTGCTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTTCCTTGTAATCATT
WI-7220b	147 A T ---	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTTATTTGTCCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140 A T ---	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTTATTTGTCCTTTAAGCTGGCAAAACCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[AT]CTAGAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232 C ---	---	---	GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGATTTGTAATAGTGACATATATATGATATA TACATACACCTCCTATTCTTAAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTGTGATCAIT CCCTTTCCATATAGGAACATAATTTGAAGTGCCAGATGAGTTTATCATGTGACGTGAAAAATAA TTACCCACAATGCCACAGTAACCTAACGATTCTTCACTTCTGGGGTTT
WI-7228b	254 G A ---	---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTAATCTATTAGTTGATTTTAAATTA CTTCTGSAATACCGAAGGGATCAGAAATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAATAGAAATGTTATCCAACCTATTAAAGATATCTCAATGTT
WI-7228a	163 G A ---	---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGCTTTGTAATCTATTAGTTGATTTTAAATTA CTTCTGSAATACCGAAGGGATCAGAA[GA]ATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAATAGAAATGTTATCCAACCTATTAAAGATATCTCAA
WI-7233c	213 C T ---	---	---	CGATCGTACTGCCAGTAGCATTGCTGTGCTGCTCCGGCTTGTGTGATTCATTTTCAATTTTACA GATGTGAACCTTATTCTCTGCTACTAATTAATTTAAATTTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTGCTGCCACCTTTTGTGGCAATATTAAGTGAAGTGAATTA GTGTAAGTATCTGTGACACAAACCACTGCCAGATAACCAAGAGGGGCTG

WI-7233b	213 T C ---			CGATCGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGCACTAATATATTTAAATATTTCTAGGAAGTCAAAAAAATAAA TAAAGGGTTAGCCCTCTACTTCTCTGCGACCTTTTGTGCAATATTAAAGTGAACGTGCTAATA GTGAAGTATCTGTGCACAAAACCACTGCCAGATAACAGAGGGGGCTG
WI-7233	211 T C ---			CGATGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGCACTAATATATTTAAATATTTCTAGGAAGTCAAAAAAATAAA TAAAGGGTTAGCCCTCTACTTCTCTGCGACCTTTTGTGCAATATTAAAGTGAACGTGCTAATA GTGAAGTATCTGTGCACAAAACCACTGCCAGATAACAGAGGGGGCTG
WI-7238	128 T C ---			GGCTACAGACAGCTCACCATTGTTGCTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTAAATCGTTAATGTATAACAGGCTTATGTTTCTGTTTCTGTTTCTGCGGTT CTGTTTAAACAGAAATAAAAGGAGTGAAGCTCTTTTCTCATTTTCAAGTTGCTACCAGTGTAT GCAGTATTAGAACAAAGAAACATTCAGTAGAACATTTTATGCTCTA
WI-7252f	520 T C ---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GGCTGCGGGCGCGGACGCCCCGCGCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCTGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252e	552 T C ---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GGCTGCGGGCGCGGACGCCCCGCGCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCTGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252d	540 T C ---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GGCTGCGGGCGCGGACGCCCCGCGCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCTGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252c	552 T C ---			CCACAGGATCCAGCCAAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GGCTGCGGGCGCGGACGCCCCGCGCTGGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGTTCCG GACACTCTAGAGAACGACGCCCTAGAGCCTGCTGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252b	540 T C ---			CTCCTCTCTGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA

WI-7252a	520	T C	---	---	CCACAGGATCCAGCCCAAGGGGCCCCCTCCGGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGGCGAGCCCCGGGCGCTGGCTGGAGGCTGCCCGCCCCCTGGTCTCTGGTCGG GACACTCTAGAGAACGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTAGCTAGACTCTCTCCCA
WI-7265m	252	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCTTT/
WI-7265l	231	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265k	121	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265j	174	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265i	227	T C	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265h	80	T A	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265g	170	T G	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT

[illegible]

WI-7301	205	A C ---	---	---	AACTATGGCAGTGGTCTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAATACTATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAAAGCAATCA AATTACJTGGACACATGAAGGGGCGAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTGCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GAJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GAJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA/GJTTTGGGAGGTCA/GAJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGAAGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	ACTCAGGAAGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---	---	---	AGACATTCGCTTCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAGACTTGGCAGATGCTCAGGCTACTATAGGTCAGAAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATAATCTGAATTTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAATTCATGATCAGATCTGGGGCAGCAACCTATAAATCA/C/CJA
WI-7338c	221	A G ---	---	---	CTCTTCTCAGACATTTGATGGGCAACTAGAAATACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTCTTTACCTTGAGC CATTTATTTGTGCAGAGAACAAAACAGAAATCAATATATAAATCAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC/GJ/TATACACACAGACATCAGAAAATCTGT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTAC/CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACATATACACACAGACATCAGAAAAATTCGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTCTTACACACATATACACACAGACATCAGAAAAATTCGTT
WI-7338	221 A G ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAAAATACCATTAATACATTTGATTTGATTTGCAAGAGGATTTCTTCA CAGATCTCATTTTTAAATAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAAAATACCATTAATACATTTGATTTGATTTGCAAGAGGATTTCTTCA CAGATCTCATTTTTAAATAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATACCTTTAAAAATACCATTAATACATTTGATTTGATTTGCAAGAGGATTTCTTCA CAGATCTCATTTTTAAATAATCTTAATGATTATTTTACTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGTCTCTGGGCTGCTCTAGCTGGTTATTTTACTTTGCCCTCCACATTTT TGAGATCCCATCTTTATCAAGAAGTCTGAAGCGACTTAAAGGTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAAGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGCTGTCCCAAGAACTTTCCCTCCAAAGATGTGTATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCTCTGGGCTGCTCTAGCTGGTTATTTTACTTTGCCCTCCACATTTT TGAGATCCCATCTTTATCAAGAAGTCTGAAGCGACTTAAAGGTTTTGAAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAAGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGCTGTCCCAAGAACTTTCCCTCCAAAGATGTGTATGTTATGG
WI-7388b	106 A T ---	---	CTTGCTGTCCCAAGAACTTTCCCTCCAAAGATGTGTATGTTATGG

WI-7398	94 T A ---	---	TGAAATCCTGGGCTCTGGCCTGTCCTGTAGCTGGTTATTTTACTTTTGGCCCCCTCCCACTTTTTT TGAGATCCATCCTTTATCAAGAGT/AJCTGAAGCGACTATAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCAATTGCAACAAGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCAGAAGACTTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	TTAGATTTTAAATTGGCAACCAAGCACTCACTGCCACCATTCCACTGCAGATCTNCTATTCTCTGG(A/G) GTTGATATGACAAGGAAACCCCTATTGGAACCAAGCTTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTCACTGTAAACATAGTTTGTNCTGGTATTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTC(T/C)GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTC(T/C)GTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCAATTTGTCTACTTCTCAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAGCAGTTGCCA(G/C)CCAGAAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGCAAGCTTCCCAACAATTAT
WI-7464b	168 C A ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTAATTTCTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAGC(A/G)AGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGCAAGCAAGCTTCCCAACAATTAT
WI-7464a	103 C A ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACTAAATTAATTAATTTCTCTATGTA GTACAACAGAGCCACAGCACAAAGAGGGTGGGCATAGCAGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGCAAGCAAGCTTCCCAACAATTAT
WI-7499b	134 T G ---	---	CAATTCTCAATCCAAOCTAGTCTGNTGCTTAACCATTCAGACAAACTCCACTTCGAAGGTTTTA AATGCAATAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAIT /GJTATAGTCCTCTTCATTAGCAATAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATATAAATTTGGAAATGAGTATGA

WI-7499a	33 A G	CAATTCTCAATCCAACTAGTCTGTGTCCTAA/GJCCATTCCAGACAACTTCCACTTCGAAGGTTTAAATGCATAAGTCAGATAGCAATCCCTTCAGTTGCCAGAGGCACATCAGTCTTTGAATGCTTCATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAACTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C	TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACACCTTNAAGTAGTCTCTGGTCTGATTGCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAGAATGAGTGAAGAGGAAAATAATCATGATGTCATGATGCAGTAATTAATGTCAGAACAAAATTTTAAATATTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C	TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACACCTTNAAGTAGTCTCTGGTCTGATTGCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAGAATGAGTGAAGAGGAAAATAATCATGATGTCATGATGCAGTAATTAATGTCAGAACAAAATTTTAAATATTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTGCGGGTTCTTGATGTTCCGAGTGCACCCAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAAATGCTAAATTG[C]TGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAATTCGGAGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C	TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCCTTTGCGGGTTCTTGATGTTCCGAGTGCACCCAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAAATGCT/CJAAATTGTCGTGAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAATTCGGAGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGCTCTGGGAGACTTTGAAGACCAGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTCTT[G]A/GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7543	162 G A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGCTCTGGGAGACTTTGAAGACCAGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTCTCTT[G]A/GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7555c	60 T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT[C]CTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCACTCTGTTAAAGCCACTTGGGTCTATAAGAAAGGAAGTAAATAATGAAGTCTGACTAGAAAATCTATTGCGAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTGATGTCATTTGAAATTCAG

WI-7555b	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAAATGCCACCATCTCCCTCAAAAATTTGTAGAGGT/CJCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCAGCTAAGTCTGCAATCTGTTAAAGCCACTTTGGGTG ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGCCATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTTTCAG
WI-7555	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAAATGCCACCATCTCCCTCAAAAATTTGTAGAGGT/CJCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCAGCTAAGTCTGCAATCTGTTAAAGCCACTTTGGGTG ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGCCATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTTTCAG
WI-7567b	290 GT ---	---	TGAGCCATCACTAGAAAGAAAGCCCATTTTCAACTGCTTTGAACTTGCCCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGCTAAAGATCAAGTGGGCCCTTGG ATCGCTAAGCTGGCTGTTTGTATGCTATTTATGCAAGTAGGGTCTATGATTTAGGATGGCCCTAC TCTTCAGGGCTAAAGATCAAGTGGGCCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63 TC ---	---	AATGATCCCCCTTTCCGTCCAAACAGGAACTGACTGGGCGAGTGAAGGAAGGATGGCAT/CJ AGCGTTATGTGTAAGAAACAAGTATCTGTATGACAAACCCGGGATCGTTGCAAGTAACTGAATCCAT TGGACATTTGTGAAGGCTTAAATGAGTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTAAAT ATTGATGATTCACCTTGATCATGCGCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGTGACCTACCTCACTGAAATCATTTTG TACCACCTTACATTTAGGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7574b	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGTGACCTACCTCACTGAAATCATTTTG TACCACCTTACATTTAGGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7574	216 A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGTGACCTACCTCACTGAAATCATTTTG TACCACCTTACATTTAGGCTGGGGAAGCAGCCCTGACCTAAGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGCTGACCACTACTCATCCCCGTTA
WI-7576c	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACACMGATGCTGTGAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGAGCGGTACTAGTTTCAGACACCTTTGGAAGTTTGT TCTGTTTGTAAACTGGCATCTGACACAAAAA/A/TGTTGAAGGCCCTTATCTACATTCACCTAC TTTGTAGTGAGAGACAGAAAGCAANNNNNNNNNNAAAAAATAAAAC

WI-7576b	168 A T ---	---	AATGATGATGATGATGATGACGACGACGATGCTGTGTAACAGAAAAACATAAGAGAGC CTTGGTTTCAGTGTAAATAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTG TCTGTTTGTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCTTATTCTACATTTCACTAC TTTGTAAAGTGAGAGAGACAAGAGCAANNNNNNNNNAAAGAAAAATAAAC
WI-7577q	77 T C ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCAATC/AATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA TAAATATGCAATCAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCAATCAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAC[G/A]TAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA TAAATATGCAATCAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCAATCAATC[G/A]TCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACCGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCAATCAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAGTTCAATTTGGTTTACACGTTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCAATCAATCGTCTCTATTCTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACACGTTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577b	117 A G ---	---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577	107 G A ---	---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAG/GJAGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7619g	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACT/GJGTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCT/GJCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCCT CGCTTCTTCTTACACAGAAACAT/GJACACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCCT CGCTTCTTCTTACACAGAAACATACACATACCG/GJAGAAACCTATTTC
WI-7619m	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCG/C/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619j	206 T G	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CGCT/GTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	---	ACAAGGCGACTTGAAGAGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCCGAGAAACCTATTTC

WI-7619c	90	C G	---	---	ACAAAGGGGAC TTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGGCCAATGGGGTCATCCGCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619b	206	T G	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTGTGTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619	189	T A	---	---	ACAAGGGGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7626d	105	A G	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC[NG]TTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626c	155	C T	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626b	28	T A	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAG TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7626	144	T C	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAAACCAATTTCTTTGGACTGTTCA
WI-7689c	134	A G	---	---	TCCCATACCGCTGATTCAGGGTCTCTGTGCTGCCGCCACCCAGATGGGGAAAGCAGGTTGGGC TCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGGAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134 A G ---	---	---	TCCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAAQA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGNATTCATATGAC
WI-7689	121 GA ---	---	---	TCCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCTCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGNATTCATATGAC
WI-7690	45 GA ---	---	---	TGGAGAACATTCAATCTTGCCGTCACATTCATCAATGAAGATTAGACACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAAGCATGTAGTGGCAAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGCCACCCAGGAAGCAC AGTCCAAAGGCTGGTCCACACTTATCAGCAGCAAACTGTCAGTTCATCC
WI-7703b	164 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTACATTGGAAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAATAAT/CJGGTCTCTCAGTTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTACATTGGAAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGT/CJAGTAAATGGTCTCTCAGTTGTTTATTTAACTCTCTAAATCT TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T	---	---	TTAAATGAGTGTGTTTGACCGTTGGGATTGGGAAGACTGTGGCTGGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACCTGCGGTCTCTGGGCTCGAGCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTAAGAGGATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGCTTCAGAGACTTCGTAATTAAAGGAACAGAGTAGAGACATCATCAAGTG GAGAGAAATCAGTAGTTAACTGCAATTAATAATTTTAAAGAAATTAAGTAGATTTTAAAA GATAAATGAGTAAATTTGTTTATATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126 G C ---	---	ACAGGGCCTTTGGAGGTGCAGCCCCACTGCTTTGACCTGCCCTTCATGCATGGAATTCCTTCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TAGGGGAAACATCCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTAAACCAAATCACTGACCTTTGCTGAGCCCTGTAATAAAAGGTCGGA
WI-7773b	237 C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGATCATCAGATTATTTTAAGTTTATCCGTAGTTTTGATAAAGATTTTCTATTCCTTGGTTCTGCAGAGAACCTAATAAGTGTACTTTGGCATTAAAGGCA GACTAGGTTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA[G/C]TTTCGACGTTTGA
WI-7774b	170 T C ---	---	TGCAACCTCTTTTCGTGATGGGAGCCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAAATCAGATCCAGCTTCGGCATTTGATCAGACCAAAACAGTCTGTTCCCGGGAGGAAACACATTTTTTAA TTACCCCTTTGCAGGCACCACTTTAATCTGTTT[C]ATACCTTGTCTTATTAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCCTTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165 G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATTGGAATAAACTGTCTCCCCCATTTGCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTTATTATCATCATTTACCA TAAATTTATTTGTCCATTGATGATTTATTTGTAAATGATATCTTGGTGTGC
WI-7785b	165 G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATTGGAATAAACTGTCTCCCCCATTTGCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTTATTATTCACATTTACCA TAAATTTATTTGTCCATTGATGATTTATTTGTAAATGATATCTTGGTGTGC
WI-7785	156 T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATTGGAATAAACTGTCTCCCCCATTTGCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTTATTATTCACATTTATTTGTCCATTGA /TJNNNNNNNGCCAAAGGCTAATCCAATTTATTATTCACATTTACCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGATCTTGGTG
WI-7789c	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCTCCTGGTGACTCGGGGCTGCTCAGACGACTAGCCCCAGGACCCATCT
WI-7789b	84 G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCTCCTGGTGACTCGGGGCTGCTCAGACGACTAGCCCCAGGACCCATCT

WI-7789	73 GA ---	---	TCCTCCCTCATCCAACTCGAAAGTCTGAACTCCCAAGGAGGGCACCACCTCTTACAGAGACTCTCCG TGACG/GATGGAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTACTCGGGGGTGTCTCAGACCACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACCTCTTCAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCACCAT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTTCTTCTTGAACCTC/GTTCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACCTCTTCAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCACCAT TACTAATCTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTTCTTCTTGAACCTC/GTTCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTCTTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTCTTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GAJTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GAJTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCTTATGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTTGCATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830c	54	GA	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTTGCATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830b	134	GA	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGAAC G/AATCCATAACTTTAGTCTTAATGTACACATTTGCATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830	44	A G	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCAATCACAATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTTGCATTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTACCCCGTAACCCCAA
WI-7865d	191	C T	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCAGGCAATTCAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTACCCCGTAACCCCAA
WI-7865c	25	C T	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCAGGCAATTCAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTACCCCGTAACCCCAA
WI-7865b	191	C T	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCAGGCAATTCAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTACCCCGTAACCCCAA

WI-7865	25:CT ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCGAGGAATTCTAGTCTCCACAAAACATCTAGCCATCTAAATGGAGAGATGATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAATCACATGCCTATGTAGGAAGTGCTATTCACCCAGTAAACCCCAA
WI-7865	191:CT ---	---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGGAATTCTAGTCTCCACAAAACATCTAGCCATCTAAATGGAGAGATGATCAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAACCTGAATCACATGCCTATGTAGGAAGTGCTATTCACCCAGTAAACCCCAA
WI-7867c	92:AC ---	---	---	TTCAAACACCTGTCTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCCTCACTAGTCCCTCTAACAAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGTTTAAATGGCCTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAACTATGTTCTATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92:AC ---	---	---	TTCAAACACCTGTCTCCACCCCTGTCAACAGCTGTGTCCTAGAACAGAGGCTTAAACCCGGCTTTTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTTCACCCAACCTGCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAAATTTCCCTGTCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTATCACTACAGGCTTTGACTCAGGTTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868c	173:CT ---	---	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTTCACCCAACCTGCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAAATTTCCCTGTCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTATCACTACAGGCTTTGACTCAGGTTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868b	173:CT ---	---	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTTCACCCAACCTGCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAAATTTCCCTGTCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTATCACTACAGGCTTTGACTCAGGTTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868	66:TC ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCC[T/C]ATTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGAAGTGGCAAAATTCCTGCAAAATGAAATCCAATCAGCACTAGAAATTTAAACATCATCTACTGCCATCTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7870b	85:TC ---	---	---	

WI-7870	76 C T	---	---	ATCTTTGCTCCGTGCAAGAAATCAGCCATAAAGAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGGC/TJGGGAATCCTATTATCAGACTCTGTAAATGAATATAATGTTTTACTCAGAGGAG CTGCAAAATGCCTGCAAAAATGAATCCAATGAGCAGTAGAATATTTAAACATCATTAATGCCCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C	---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCACGCATGCTCCCTCCAAGGCTGTCTCTCCAGAGCACAGAAG
WI-7889b	54 C	---	---	TTAGGTCTCATGCCACTCCGCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCCGGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCACGCATGCTCCCTCCAAGGCTGTCTCTCCAGAGCACAGAAG
WI-7894c	142 A G	---	---	AGCCAGCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTAGTAAATTTGCAATTTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCCGTATAGAGTATCCATA
WI-7894b	142 A G	---	---	AGCCAGCCCCAAATATACTGTTATCCAGAAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTGTGAATTTATATTTGCGTATAC ATTATC/AGJTAGTAAATTTGCAATTTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCCGTATAGAGTATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCTCAGATTTGAACCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAGAAATC

WI-7900d	128 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAATGCATTGATCATGAATAGGAGGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAT(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGAC CCTTTTAAACAACCACTCCAGGCCCTTGGTTGGGGTGGTGGTATTTGGGGCAGCGCCGTTGGTGGT CACTCAGTCGCTCTGCTGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T	---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAT(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCACTTTTATAAACATGGTAAGAC CCTTTTAAACAACCACTCCAGGCCCTTGGTTGGGGTGGTGGTATTTGGGGCAGCGCCGTTGGTGGT CACTCAGTCGCTCTGCTGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T	---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCAATTTTATAACATGGTAAGAC CCTTTTAAACAAACTCAGGCCCTTGGTTGGGTCGCTGGTTATTTGGGCGCGCCGCTGGTCTG CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCAATTTTATAACATGGTAAGACCC TTTAAACAACTCAGGCCCTTGGTTGGGTCGCTGGTTATTTGGGCGCGCCGCTGGTCTGTCAC TCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCTGTT
WI-7926c	150 C A	---	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATG ACTTTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTC ATTTACAATGCAATACTTA[C/A]ATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A	---	---	---	CATTCGGCATCTGTCAACGAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCCAGTGTGCCACCTG
WI-7947	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCGAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCCAGTGTGCCACCTG
WI-7963b	145 T C	---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAATGCC ACAAATTTCTATTTCTCTCTTAAGTATTAATGAGTTATTTCTGCTGCTAAAAAGTGAAGAAAT TGAGTGAATGAT[C/A]ATTTTGTAAATTAAGGATAAGATCCCAAGTTATTTTCCCAACTCTTTGTTCCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTCATTAAGGCGAGAGACGGGAAAA

[illegible]

WI-8021b	57	C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATTCATCTGGAAA[C]TGAATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTTGAGTGATCTCAAAGTCTGGTAGGCATTGGA ACTGGTCCCTTACCTTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAAITCGGTGAATTGCCA
WI-8021	57	C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATTCATCTGGAAA[C]TGAATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTTGAGTGATCTCAAAGTCTGGTAGGCATTGGA ACTGGTCCCTTACCTTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAAITCGGTGAATTGCCA
WI-8024c	206	A G ---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACCTCCCATGGGAAGACAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGAAAGAGC
WI-8024b	206	A G ---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACCTCCCATGGGAAGACAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGAAAGAGC
WI-8077	167	A G ---	---	GAATGAGCCTTCCTAGCGCCGAGGAGCTGCTGCTGTTGTGGCTGCACATTCATATGGAATGC TTTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACCTCTTCT AAGGAGCTCGGGGTGTCATGCCCTACAAACQ[A/G]TAAATCTCATCAGATGGATTTATTTAACGTT GTGTAATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAAGGGAATAA
WI-8118f	114	GC ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGG[A/G]TGACCACCTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTTGCTGCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGG[A/G]TGACCACCTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTTGCTGCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATTTTGGATTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTTGCTGCTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTGTGTTGTTCTTAGCCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGATTTTCTGATTTCCCTGCTCCTCTATCTCCT AAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/T/CJGGCAATACAGAATGTAGCTGTGTTGTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGATTTTCTGATTTCCCTGCTCCTCTATCTCCT AAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGAGGCTCGGGAAG AGGGGTAGGAGACCAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGAGGCTCGGGAAG AAGAGGGTAGGAGACCAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGAGGCTCGGGAAG AAGAGGGTAGGAGACCAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGACCAAGGTACCTCTGGGGCATACAATGGCAGGAGGCTCGGGAAG AGGGGTAGGAGACCAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTATCTCTAAGGGG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGTCTGTAGTCTTATGATGATCTAGAAGGACACTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTCTGACCTATTCAAATAGGGGTAACTACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTGGGTCTGT TTCTATCTCTGJTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGTCTGTAGTCTTATGATGATCTAGAAGGACACTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTCTGACCTATTCAAATAGGGGTAACTACT

WI-8321	178	G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAAATGTTGCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATCTAGTACTCTGAGAAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAAATGTTGCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATCTAGTACTCTGAGAAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-832b	123	A C ---	---	---	TATGACTCACTTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGCCAAGCCAGCTTTCCCTCCCTGTCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	---	TATGACTCACTTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGCCAAGCCAGCTTTCCCTCCCTGTCAGCCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTGTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAGAGGAGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAAGGCCCTCTCCAACACGTTGGGG
WI-8378	308	T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATATCATGGCAGAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAGAGGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAAGGCCCTCTCCAACACGTTGGGG
WI-8426	184	T G ---	---	---	TTTAGCACATATTTAGCATTAAAGCCTCAACGATACAGCAATATGTTACATCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACCTCGACTTGGCCCTAATAGGATTTGACCNNTAA GAGNTTCTTTTCTGTGGANGGGGTGGCTTGTCTGAACTCCATTCTGTG/GCCTTGTAGCTGGTG AGGCTGGAGTATGGANGNCCCGGGGGCCCTGGGNATGNATCAGTGAG
WI-8450h	61	C A ---	---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTCTACATACACTC/AJCA TCCTCTATCTTAGTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108	T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JITTTAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JITTTAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JITTTAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108	T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTTT CTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61	C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTTT TCTTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55	T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTTCCTCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60	A G ---			CAAGGAAAGCTGTCAGTCTTCATTAACCTTCAAGAGTTCACAAAATACGTTATTTTAA/AGJCTA CAATTCAGATTAGCATCCAAACCTACAACATGATGATACATTCGTACACACCATACAACCTTCAC ACCTGGGTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAACAACTTTATTTGTCACAGT GACATCCATCCGCCAGACTTAATGTTATTAAGCAGCTGAGCAGAGTTCCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATCTTGAAGACAAT[C/G]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATCTTGAAGACAATATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATCTTGAAGACAATATACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGAGGTAGTACTTAATTTTGATAAAAAAAT TAAAAAGCAT[G/A]ACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAATATTCTCCCTTTGTTTGTCTTTTAAAAACATTATTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTTACTAAAGCCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGCAGCTCAGTACCTG[C/T]GTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTTACTAAAGCCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGCAGCTCAGTACCTGCTGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAAAGCTTGATTAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAGANCATT TAAAAAAAT[C/G]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGNNCCCTACTNTTATCACTGTGCTCTTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75	T C	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGNAACCTTACCATTCCATAGACTATAAAGANCATTAT TAAAAAAATG/C]CCTCTAAAGNGACACATGCCCAAATGACGANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGNCCTTACTNTATCAGTGTCTCTGCTCTTTTGCTACCTA TGNGACGACACTATCTGTGGCAATATTGT
WI-9497b	185	A	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTTT GAGATAAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A	---	ATTAAAAATGTCAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTTT GAGATAAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAGGCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A	---	GTGAAAAAGTTTCTATTCTCATCCATCATACATAGATTGTGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAAGTTGATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTGTA/C]A]AGTG AAAGCTTTCAGCTTGGAACTTGTCAAGGCCAGCTGCATGCACATATAT
WI-9523a	47	G A	---	GTGAAAAAGTTTCTATTCTCATCCATCATACATAGATTGTGCTAAGGATCATTTTGGAGAAT GTGCAGCATTCAGAAAGTTGATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGTTGATTTCCACACATTGTACAGTGA AAGCTTCTCAGCTTGGAACTTGTCAAGGCCAGCTGCATGCACATATAT
WI-9554	202	T C	---	AAAAACAAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATGATGCTGCTTNCITAGTTGTTATGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GT/C]GCTGGATACCACTAAGAAAGTCTACTGACGCCATGTTGGTTATGATTTT
WI-9555	97	G A	---	CCAAAAAGCCAAACCATTCATATGATGGATTTCATAAACATTTTATGATCCTTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G]A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAGGCTGTAACCTTTTNCITTCACATTGATCACA
WI-9625b	172	A T	---	TTGAACATTTAATGAATGACAAAGACATAACATCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACATAGCTACCATATATTTGATCTNCITCTTGGGAAAAAACCTTTGGAAAAAAAACACGCACA TAAGTATCATAACTGAGGGTGTGGACAAAGTTACTTCTA]G]TTTACCATTTTATATTTGACATAA AGTAGCAGACACTAGTTATTTTCAATTTAAAAAAAACACACTGCACAAATCTTTTC

WI-9625	172 A T	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGGAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGTGGACAAGTTACTTCT[AT]GTTTACCAATTTTATATTGACATAA AGTAGCAGAGACTAGTATTTCATTTAAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T	---	---	TTTTCTGAGATTCAAGAGCTACATTTTGGTAGTGTACTATACCTTTTTCCTCTTTCA ACATCTTTTGTACATTTTAAAGTGATGCTCTTGTAAACAGTGTATTGTAGACCTAAAAATCCAAGCT TACAAC[CT]GTCTTTACCTGATACATTTATCCATTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676m	184 G T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGG[CT]CATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676l	84 A C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676k	202 C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA C[CT]CAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676j	92 C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676i	173 T C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9676h	134 C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGAGG C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676f	184 G T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGC/T/CATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676e	173 T C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCC ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676d	134 C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA/A/GJGATGTGGCTTTCTGCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676c	114 A G ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA/A/GJGATGTGGCTTTCTGCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676b	92 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT
WI-9676a	84 A C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAICCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJATTACAACATCATTTGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGTTCCTACTATGTGAGTATCTA TCITTTATTCTGTCCCTTAITGGTGGGCACATGICGTATGCTGTCC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJATTACAACATCATTTGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGTTCCTACTATGTGAGTATCTA TCITTTATTCTGTCCCTTAITGGTGGGCACATGICGTATGCTGTCC
WI-9756	47	A ---	---	ACTGAAATGTAAATGGCCAAAGGCCACCCAGGACCTTAAATAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACACTACAAAAGCATCTAACAAAGAGCAGGATGTGATGTAATGTGCCCTTATCAGCTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAACACACAGATAATACACTTTTGGGAA ATTCCACTTAACCACTTGATCTTCACITTTTATGATTTTAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATGAATAAT TAGGAAACTGGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGAAGGTCAATTTTATACTATTTA A/A/GJTAAATAAATCTGTGAGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTCTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCGGGGAAAAATGGATACTTTCATATGCTCTGTACCCCACTATAAACTTTTG GTTCTCATGGCACCATTTTCAATTTTGGCTTCTCAGTCCAGTACCAGTGTATTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCGCTCA AAG-AATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTGCCCTCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTTTC/AJTGATCCCAAGGAGGA CTCAAAAAAAGTGGAAATGGGAGAAAGAGGACCTGGAATCGGTGTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCTATTTTGAATGAATAAAATATAC/A/GJTGATGATGATATATATATTAACACTT AGGATTATATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	G A ---	---	GAACATAACACCTTTCTTGATGGAATTTTCTTGATTATGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTGTCTGTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTAATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/GA/JTGACATAGGAATACCTACATATTTTG

WI-9880b	157	C A	---			GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C]ATATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---			ACACTGCAGGCCTCCAAATCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAAACACGCCAGTTATCACAGTTTCTNTTTTGT[C]CACC ATTTCCATAACAAAGAAAGCTACACAAAATNNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G	---			TCCCTCAATGACAGATGAACATAATTTTCTCTGGGTAGAAATACTTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G	---			TCCCTCAATGACAGATGAACATAATTTTCTCTGGGTAGAAATACTTTATGTCCTTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A]GJTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A	---			ACAAAGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C]A[CAATTTTCAGNAAACAAAATCAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCCTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAACTGACAATGGGTGTGCCC TACTGAGCTTGGGCCAGGTGTACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C]TTTGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTTCTTT[G]TAAATTTGTCAGTTT ATTCCTGGAAATCTTTGAGTTAAATAAGCATCTAGGACAGCACCTCAGGACTACAGGCCCTAAA GAGAAATTCCTCAACCAACAAGTGCTGTAACCTCTCCCTTCTGTCATTTGGTTGCTCTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTTGGAGTGTCTTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TAATCTTTTATCTCTGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAACACAGAGCTACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTGTTTGGACAAAAATAACNAGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGCTCCTCTCTCACANGCTGTATTACCTTTCAGAGCTGAGTGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCTCTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANAATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGCGAACTGG
ESTC129	20	---	---	---	AGTCACCATGCCACGCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTAAGTGCCTTAGCAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCANAAGTCTCTCCATGTGCAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGTCAGAGTTTCTCAGAGAGNGGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTGCAGGAAGNAGAGGAGGCCAGCTTCTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCATTCCCTAACAAACA
ESTC143	29	---	---	---	GTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGIGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTAGCAGCATTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACAGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATGCTGTNATGAGCGGCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCIGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTTATCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCAGGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCTGGCTGCTCGGATGGAGCGGGGGCCCTCA CCACCCTGCT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNACGTTGGTCAATTTAGGACCGGTCTGGTTCTGCA GCTTGAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCACAAGGACAGGTT
ESTC160	38	---	---	---	TTCTAGCATTGCTGGTGCACTGGGGGCTGAGCTGGGNGCAGTGGCAGTGCTCACTGGGCGCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTCGTCGGTTTGCAGTTGCTGTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATAATTGGTTTTGTAAACNGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGTGCCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATTCCTATTAATAACCTTTTAT TCTCTTTATTCCCATAAAAGGCCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTTCATTCAGCTTG ATTTTACCTCA
ESTC187	24	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	TCTATTACAGGGTTATGTCACACCCNTGTCAACCTCAAAACAGATGATACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	AMAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAATACCACCTTCCCTAACCTTATCAGICTAGTAAAGCNITTTCAAAGGAGGAAAAATGGGTTAC CTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCTCCNCGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGGCTGCAACAG

ESTC201	35	---	---	---	TCTACTTGGGTAGTTTAGCAACATTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGAGGACAGACGCGNCAGCGGCTGGGTGGCGGCCOCAGAAAGCGTGGCGTGATGTT
ESTC203	27	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGTACT
ESTC210	29	---	---	---	AAGACAGTTGCA
ESTC212	27	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAACTCTGAGAGGGATAANAGCAATAACTATTGTTAAAAGC
ESTC214	21	---	---	---	CTAAGAGTGA AAA
ESTC216	49	---	---	---	GATGAAGTGGCTTCTTTGGCGAAAGGATNAAGAAAGTGAGTGACGTGACCTGTG
ESTC217	28	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	TCAAGTC
ESTC22	41	---	---	---	CTCCAGAGTCCTCTCTCANACCAGGGGCAGGAGGAGTTAGGGAAT
ESTC223	27	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTTAATCACAGGTATNTTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	CAAAAAGACCA
ESTC225	20	---	---	---	TTTTGTCAGTAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATAACAAAGTTTAT
ESTC23	27	---	---	---	AAACACCCCCA
ESTC230	43	---	---	---	GTACACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	GCAAAGGAAGC
					TCATTGAAGAAATTAAGGGTTTATTCTTATTCTTAATTGNGAGAATGCTTAATGTCACAGGCTACA
					TAAGGGCC
					CITCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCITGATTTAAAAAACAGAAAGGGGAGGAGGA
					CGAAGGTAGATTCCCTCACATATTACAAAATACANAAACACACACACACACACACA
					TGCACGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA
					ATGTGTAGGATCG
					TTCTACTTTATTTCATATTCACCACACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
					TCCTGAAAGGG
					GCTTCTCCACGAATTTGAAGACATATTGGCTGACCTGATACNTAAGGAGCGGCCAGAAATTAAGA
					CAAAAGGGTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNITTTCTTCCTCTATTCCTATAAAAAAGGAAGCAGAAATCTC
ESTC3	20	---	---	---	CC CAGACATGACCTACCGTCCCGGCCCTCAATTCATATTTTATCTTGAGCGCGCTGGTCAGGTTTGAT
ESTC31	32	---	---	---	ICGCACACTCC ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATAACAAAG
ESTC33	25	---	---	---	CAATTTCTCTCAGA AGCACTTCCAGCTCCTTGACGTTGNGGACACAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACICAGAGCCITGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAAGAAACCAAT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCICTCATCATCGAGGCTATATATTA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCGTGTCCCATGGCCAGGAGCCACTGGTGGGNNOCGGGCAGATG
ESTC56	45	---	---	---	TTTACCCTGT GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGAAAGGACACCA
ESTC57	20	---	---	---	AGT AAGTGGGCCCTCCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACCTTCTCAAAATNGTCCAGACTTCAGGAAAATGATTTCC
ESTC6	27	---	---	---	ACATGGTAAGGCC TCTGCAGCACTTCACCTACCAATGAGCNITTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATG
ESTC61	57	---	---	---	TGGACTGAACCG AGTGATTTGGCTAGCGGTGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC
ESTC63	20	---	---	---	ACCCACTCAAG ACAGACACAGCATCACACANAGGGCCACGGAGGGTCTGGGAGACGACACTTTTTCCTCGGAAA
ESTC69	20	---	---	---	GGCAGCTCTAATC GAGAGGTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT
ESTC7	45	---	---	---	CACCTTGGCTAA AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACT
					G

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNITTTGGCGTGACGCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAATCTAGAACAAATCAAATATTCATCACNTTTGGGTTGAAAAGTTG GAGA
ESTC74	49	---	---	---	ATGACTTTCCTGTCCCATCGGAACACAGAGTTTCCCAGNGAGCCCTTCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGATAAGANCCCCACTCCGCATGTCGCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTCCATAAANCTGTCTGTGTTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCTCTCGTCTGGCAITCGTCTCCTCCTCNGGCCAGTGTCCACCAAGTGTCTTCCCGATGAT CTCCCTCCTCAGTTCACAGTGAGACTANGGAGATTAGGGCAGGATCC
ESTC89	22	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAAGTTGNAGACGTCTATTAGTTTGAATTATCTGTCG
ESTC90	33	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATICA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAAGTGTCTCCACCTGCGCAG ATTCTTATCAATGATCTTTACCTAAGAACAGCAAGATTCTGGCAAGCAGCATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
ESTC93	29	---	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGCAGTGGCCCTATTACAGTAGCCAAACGATGAAAACACCCCAAGCTATATATACCA GATGAAAGGATAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
ESTC95	32	---	---	---	CAAAATACCTGGACTATCAACCTTGTGTGTTAATCCCTGCAGCATCAAGGTTAATCCATCTAAGTGAC ATTTTGAATTCACGGGTGCCACCCCAATCATGCCAGCTTGTGATGATGAATGAGATATACATTT ATGCTGACCTCCCTCAAGACTGATTTTTCATGCTGCGGACTACAATATCTCAAGGAACAGCAATG TCAACAGGGTCTGGAAACACAGCCCTATCTGAGTCTTCGGCTCCCTCC
DWU-100	127	CT	---	---	
DWU-177	77	AG	---	---	
DWU-286	213	AG	---	---	

DWU-252	94	A G	---			AGTATACAAACATTTAAGCTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCTCAAGTGTGAGATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTGTGTA AT
DWU-330	85	C T	---			GAACATTCCTCTGCAGCACCTTCACTACCAAAATGAGCATTAGCTACTTTTCAGAAATTTGAAGGAGAAAA TGCATTATGTGGACTGAAC/TCGACITTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTCTTTTGCAA CAAGACAAGCAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTTCAGAAAA CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAAIGCAATCTCCCT
DWU-370	231	A G	---			GAAATGTTAATTGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTTAAAGAG AAGCATCATTTCCCAACACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTCTC ATTAGACGGTACCAATTCAGTGTCTGTTCTTGA/GGCATCTATTTCCTCTGTGC
DWU-1537b	89	A G	---			CTCTTAACITTCAGTTCCTCATCTATAAGAATAAGGGATTGAGTTGTGATCACAATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/AGTGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---			CTCTTAACITTCAGTTCCTCATCTATAAGAATAAGGGATTGAGTTGTGATCA/C/ATAGCTCAGGTA ATCCAGGACCAAGAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---			ACCATCTTACTATGCGAGGTAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCTCGGCACCTGAGCTG/C/GJAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ADAA	184	A G	---			ACCATCTTACTATGCGAGGTAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATTCAGGGTCACTGTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCTCGGCACCTGAGCTG/C/GJAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ANT1	160	T C	---			TCTCTGTCTACTCTACTCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTATGGAGACCGCAACTGAGGCT/C/GAGCTCAGATGATCTCTGT
EST10398						TGCCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTCCAAACACGGAGAAG CATTTGTTTCTTCGGGCCAAGAGGTATCTACC/AG/ATAGTGTCTATTAGGCATTTG
2b	168	A G	---			

EST10398 2a	147 C T	---	---	TGCTGGGTGGGAAGGCTGCAAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATGTTTCTTCTGGGCAAGAAGGATATCTACCAATAGTGTCTATTAGGCATTTTG
ESTD-C7	14 G C	---	---	ATAICGTGGCCTTAGCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACATTTCGAAGG ATAATGGGGCAATCACCTTTCTTTCTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A	---	---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACCCGAG/CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G	---	---	CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACTCTATAGTGGGGTCG TATTCGTCCACAAAGTGCATCTGGATCAGCT
ESTD- HRASa	37 C T	---	---	CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGGCTGGCGCCAGGCTCACTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G	---	---	GGAGGCAGGAGGTGGGGAGGGGCTGCTGCTGCTCCAGGTCCACAGACCAGAGAGCGGCCTCAGTG TATCCCCACCCCCAAGTGTGGGGCGCTGGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G	---	---	GTGACCTTCTCAGTTAAAG/AACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T	---	---	CCAACTGCTCAATTTAGCTTTCAGGTTTAACTCTGATTAATCTTTCTATTCAATCTCTGTA AAATTGAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109 A G	---	---	CAGGTGAAAGGAGCTATTTTGGAGGCTTAAAGAGTAAAGAACTGTCCCCAACTTGTGGCTGAC TTTATGGCTAAGAAATTTTCACTGGATGCATTAATAACAAATAGTJTACCTTTTGAATAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGATCCGTACCGTCTGACGTTTTTGAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	121 C T	---	---	GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTGCTGAGAA GATTGACAGGTTTCAAGCAGGCTGTACAGGATGGAAGACTGGCTGCTCCCTGA/CTGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCACACCTACGTCCACTTCCAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTAGTATCC
ESTD-AK- 168	31 C T	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTTTACAGCTGTGTTCTCATGGAGACAGGCTTCT GCTCATTTCTGG
ESTD-ALB	180 A G	---	---	AATCCCAGCAGCTTTAGGAGGCTGAGGAGGATATCACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTATAAAATACAAAATTAGCCAGGATGGTGGTGCCTGT AATCCCAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGAGGGGAG/AGAGGTTGTGGTGAGCCGA GATGGACCAATTGCACTCCAGCTGGGCAACAAGAGTAAACTCTGCTTC

EST70523 3	182 G T ---	---	TTCCGCCAGCCCCCATCTTGGACCCCTGTGCCCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCGGTAAACATCCGGCGGGCGCGCTCTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCCCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCT[G]TCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101 C T ---	---	CCAGTGTGTGGACGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGATCTTTTGAAAC CGGGAGGGGAGGTTGCAGTGAGCTGACATG[C]TGCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGAG[C]CTAGAAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTGTCACTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---	---	AGACCATGAAGGAGTTGAAGCCTACAAATCGAACTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGCACGGCTGTCAAGGAGCTGCAGGCGCGGAGGCCCGGCTGGCGCGGAGATGGAGGA CGTCCGCGCGCGCTGTGCAGTACCGCGCGCAGGTGCAGGCCATGCTCGGCGCAGACACCGAGGAGC TGCGGGTGGCTCGCTCCACCTGCGCAAGCTGCGTAAAGCGGCTCTC
EST43211 8	132 C ---	---	CGCTGGTGCAGTACCGGGGAGGTGCAGGOCATGCTCGGCAGAGACCGAGGAGCTGCGGGTGG CCTCGCTCCACCTGCGCAAGCTGGTAAGCGCTCTCCGATGCCGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGGCGCGCGCGGAGGGGCGGAGGCGGCTCAGCGCATCCGCGAGGCGCTG GGGCGCTGTGGAAACAGGGCGCGTGGCGGCGCGGCTG
ESTD- ARSB	126 A ---	---	GGAAAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATTTGACCCCAAC
EST36770 4	144 C ---	---	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGATCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTTCCCTTTCTCTGATCAT TCTTACAAGTTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAGTAATTTGTGAAGAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATGAAGAGAAATGCAATATGTGAGCTGAACCCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTCGCAACAAAGACAAAGCAAGCC
ESTD- BA511	29 A/G ---	---	GGGCAACATAGTGAACCCCATCTCTACA/GJAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAAGCAAGATGGTCCACTGCA

ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGG[C/T]GGATACAAAG ACAGGAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTCITCAATTAAGTCTCTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGGCTTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAACGTTGTTCCCAACCCGA GGTCGCTGTTTGAGCCATCAGAAGCAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---			ACAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAACGTGTTCCCAACCGAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACACGCTGGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTTCTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGCT TCTGCTCTCGAACCCAGGGCATGGAAATCCAGGACACAGGGGCTGAGGGAGCCAGAGCCACCTG TGACAGGTGAG[C/T]CTACATGCTCTGTCTTGTCAACAGAGCTTACCAGAGGGTCTCTGCTGCC ACCATCCTCTATGAGATCTTGCTAGGGAGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGTCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGTTGCATTCAGGAGTGCTGTGGAGTTCTGCTCATCTAGC[C/T]TATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCT GCTTCTCCTGTTCACTCTGATGGAAGTCTCTCAACACCAATTCATACC
ESTD- D4S338	59 A T ---			TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGAGGTATATGA/ATATGTA TTTCTTAAACAATAAATCTGAAAGTCCAAATTAATCTCTGATCCATGGAGTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTATCAGAGCCCTTGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAGAGGAATCTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---			CAGCCAGCGGTGTCAGGTGTACCATCCGGCAGAGAACAGGTACGCCACCACTATG[C]AG[C/A GGTCTCATCTTGAAGTGTCTCAGGGTTCCTCTGGCCTGAGCAGGGCGGAGAGCATCTCGG
ESTD- D11S1873	40 A C ---			AAAAAACATTTTAAACCTTTTCAATCATATACACATA[A/C]ATTTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATGCAATCTAAATGTCACTAATGTAATGCAAGTTCAACAG ACAACITTTCCCAAGCATCTACGATCAGAAAGGTCAAAATAATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---			CATCCCAAGCCCATCTCTAGCCACTGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCGGT CATGCTGCACACATCCAGGGGGGCCCTACCTTTGTAGTCATGGGAAGGCTCCTCTGGGCGGTG GGGTGTGTGGCTATGTGGTGTCTGTGTAGAG[C/T]GGGGCTTTGTTTCAGTTGCACACTATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T	CATCCCCAAGCCCATCTCTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTAGGGCCGT CATGCTGCTACACATCCAGGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTGTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCATATTCGGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGAGGAGAAITGCTTGAACCCJA /GJGAGGCAGAGCTTGAGTGAGCCCAAGATCACACCACCTGCACITACAGCCTGGGTGACACAGTGG GACTGCTGCTCAA
ESTD- D3S11	44 G	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCAGCTTATTTATTGTTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTAATGCTGATGTTGCTGATGTTTCJA/GJGAGGCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTAAATTCAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGATTTCCC AGAAGTGAACATACCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGCTCTTTATTGGAAGGATGCTGCTGGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGATTTCCC AGAAGTGAACATACCTCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGCTCTTTATTGGAAGGATGCTGCTGGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJA/GJGCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGACA GAATGCTGATTJA/CJTGTGGTGGAGAACCAACTTCTGGCCTGTGGGTAGGGGACGCTGCTCCAAAG ACCTCCTGATTTGAGGAAGGGGAGCAGAGCGAAGAACAGAGT
ESTD-DMa	66 C G	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCCTCCACJ GJTTCATGGGTGTGGGGCTGGGACCTCAGTCTCCCTGGGAGAGGAGGAGGTGGGAGGGAGAGA CAGAACTGCTGATTATCTGTTGGAGAACCAACTTCTGGCCTGTGGGTAGGGGACGCTGCTTCCAAAGA CCTCCTGATTTGAGGAAGGGGAGCAGAGCGGAGAACAGAGT

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTCTATTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAACGGTACGACCCCAACCTGAACCTCGAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGCGCTTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTTGGTCAGAGGGCTGCCCGCGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGAGCCCGGTACAGCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACACCGGTCTCCACAGCACTCCACAGCCCGCCCAACACAGAGAAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTGCCCCACAGGTGTAGTTGAGGTGGCTACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTAGGAGA
ESTD- EPB82	93 C T ---			TCTTTCAGGATCCGATCTCGCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGTGGTGGTCAGTGCTCTGGGGCCGGTGCAGACCCACCGCGGCTGGGAGGACTCA CCCCGCTCACTCCGTTCTCGAGCAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G ---			ACTCACAGTCTTTAAGTGAAATGGTCGAGAAAGAGGACCACTGJGGAGCCCTCTCTGGCGCTG GGAGTCCGTGGAGCGGATGTTCTGGCTGTTGAGATCTCAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTGAATTTCTTTGCTTTTGCCTTTTGCACCGAGGACAGCAATGCAAAAACCTTTTGAG AGGGTAGGAGGGTGGGAGGAAACACCATGTCTTTCAGAAAGTTAGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTTACAGTTTGAAGTTTATAGTTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTTAAGJGTCAAACCTCATTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTGACTTTATTTCTCCTCAITGCTTACCCTTTACAGGTGTTAATATAGTGAAMG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACAAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- G00H	200 C G ---			CCGACACCGGTGAGTGTGGGTCGGGAGTGTGGAGGAGGAGGAGGAACTGGGGGTTAGGGACT TTCCGGGGTGAATTTCCGCTTCTGTGCTTGACAGAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGAACCTCTGTGTCGACCCGTGTCTGCTGCCCTGTTCAGCTGTCTGTGCGCGCAGTCT GIGACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A/G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGCCACTCTCTGTTCAACCATGAC AACCACAGGCCCTCTCAGGAAGJACAGATGAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGGGCCCTGAGCCCCAGGAGGAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ...			GTGGGGCAACAGTGGGAGAGAGAGGGGGGCGGTATAAAAGGGGGCCACAAGAGACCGGCTC[AT] AGGATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ...			GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[AG][GGCATCA TTGAACCAAGTTTCCGTCAAGACTTGAATTCAGGTAAGTGCATGGTTCCTAGG
ESTD-HT2	154 G ...			GGGTAAATTTCCGAGCACTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGACAGAGAGAAATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACCTT
ESTD-HT5	149 C ...			AACACAAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGAGCCCTCGTCTGCTGTTGTTTTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA ACATTTGCTGCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ...			CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCCCCCCTCTTCTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAGAG[AG]CCCCAGA AATCACAGGTGGGACGTCGCTGTCACCGCATCTCCCTCTCACGGGAATTTTTCAGGGTAAACT
ESTD- IGFBP1	43 C T ...			ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGTGCT[CT]CTGGGAGAAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ...			TTTACTATTTCAATGGATACAGAAATTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTCCCTACATTTGTTGAGTGACGGGGCAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAAGAAAGCAATATGGAAGATGATATCTATGGATACGAACTGAAAGT ATGTAATATCTTCAAAAATACTATAAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	110 A G ...			CAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTAATTATTTATTTATTTTGT AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGCAGTGG[AG]CAATCTCGGCTCACTGCAAGCT CTGCCCTGGGTTCAATGCCATTCCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCAACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ...			CCACTTACAGATGGAATAATGGGTACAATGAAGGGCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCIC[AG]GGAGCTCTGTCAATTGCAGG
EST74082	134 A T ...			TCCAGGTGGCTGACCCAGCCAGCTCTGCAGCAGGAGGAGCGTGGCTGGCTGGTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGACCGCACTGGCTTCAAGCTCAGCCCTGCTGCTGCT[AT] TCCAGATCACTGCTCTCTGCCATGGCCCTGTGGATGGGCTCTGCCCTGCTGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGC

EST45311	151	CT	---			GCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATGACATCTTTTAGT GGATAGATGCACACAAACACAGCCATTATGGGAAAGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTTCAATTAACAGCCCTTATTCAATGGCCCTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258	80	AG	---			TGCCCCATACGCGCGGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCAGCCCTCAAAATGACAGCCATGGCGCGCGGTCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAGGCTTGAGGTTGGT GAGGTTAGGTGGGTCTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216	26	AT	---			ATGCAGGATGAAGGTGGACAGGGAGGAT/GAGGGCAACCTGTCAATCCAGGGCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGACATCAGGG
EST62782	149	GT	---			ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC/GTAAAGTCCAGTATCCAGAGTTTTGGTTTTTGAAGTGAAGTGAAGTGAAG AAGAACTGAATACCTAAGATTCTGCTTGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183	CT	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAGTTTAAACCAGTATTGATA
ESTD- KRT10a	133	AG	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTAAT GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTTTTAAATAGT TCTGCCCAGATACATCTCCCTATATAGTTTAAACCAGTATTGATA
ESTD- KRT8b	231	CT	---			ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGAGGGCCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGATGTTAAGTACAAAGTGAAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21	CT	---			ACCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGAGGGCCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGATGTTAAGTACAAAGTGAAGGCCCATATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
EST75099	82	CT	---			CACCTGTGTGTCTAGATCTCCTCAGTGGCGCCCTCTACTGGTTGACTCCAAACTTCACATCCATCTCA AGCATCGATGTCAAC/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC CCTCTCCTGGCCGCTTTGAGGTGTGG

-185-

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACCGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAAAATTTCCAATATGATGCTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GAGGGCTTCCCTTACCACCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCCCAATCTTGCGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCCACCGCTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTCTTACCCATTCACTGAAAAGGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGCACCTCACCTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATTCAATGTCTCTCATCTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTTCTGTTTTGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCAACAATTTATTAAAAATTTTCACTG
ESTD-MCC	45 C T ---	---	TTGTCCAGAGTGTGCTGATGCTGCCTCCCGAGCTCTGCTCCAG[C/T]GAACCTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTCTGAAG ATCTTCAACTGCTAGAGCATCTGGTCCCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAAC[T/A/G]TACCAGATCCCACAGACTGATGGCTGGT AAGATGGACTTGTATATTGTACAAAAAAAGTTTATTTTTAAAAAAAGAAAAAGAGAAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCCCAAACGTTATTGTGGT AGGATCAGCCCTCATTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTAAACCTCACCTTTGTGGGGTTTGGAGAAAGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCTGCTTGTCTCCCTGGCTGTATCTT[C/A/G]GTACTGCAAGAGAACACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACTTTTTGTGTGATTATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTAACTTTGGCAATAGCATTTG C/TATTCCTGTGGTTTTTAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACCCACCCAGCACACCTCCACCTCAGCCAGACAAAGTTGTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTACGCCGTGTATCATCGAGCGGCCGGG CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAH1	100 A G ---	---	

ESTD-PAR	120	A	---	---	CTCTTCAGGAACACCAGTCTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74	A	G---	---	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACATTTTCTGTGTTCTAGAACGTTTCTTAG
				---	GACTGGCAGTTTAAAGCTTTCACITTAGGCTTCTGTATACCCATGCC
				---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
				---	CTGGAGA[AG]GAGCGTGGCGGAGACCTGGAAGGCT
				---	GGAAAGATTTAAGAAGCTTGATTGGA[CT]AATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC
				---	TCTGCCCTGAGTTACAACAGAACTCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
				---	GGAGAAGTAGACTTTAAAGGTAAAGAAAGTAGTTATTTT
EST54045	6	39	A	G---	GGAAATATAAAATATTTAAATACCTCCATTTTCT[AG]JTCCTTTAGTGAAGATGATACCTGC
				---	AAAAGACATGGCTAAAGTTATGATTGTCATGTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
				---	TCTGTTAAGTAAGTACTGTTTGGCTTGGAAITGGATTTTAAITGTTGACTTTATCAT
				---	ATGAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTTTA
ESTD- PXMP1	88	A	G---	---	ATGCAGAAAGAGGGGAAAA[AG]GAGCGAGCTGTGGTGCAAGGTGTTTCTCAAGGCTCATAC
				---	AGATTCTGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTTATGAAATTTATAATCTT
				---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGTGTGCTGGAGAAGAGCGTGCCGGAGACCTGGAAGG
				---	CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGGAAAGCCGAGGCGCAGACGCGAGG
				---	CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAAACACTGAGAAATAGTGCACT
ESTD-RDS	127	A	---	---	CCAAAGAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
				---	TTGGGAAGTTAGAGCTATATTAAATTTACGGAATTTACTAAGGCAGGACACAGAGGCTTAAATTGAAAA
ESTD- s14544	94	G	T---	---	TATCCCAAAGTTGAAATGTCACAGTTG[CT]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA
EST52908	0	45	A	C---	ACCTCT
				---	ATCACAGGTCCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG[AC]JGGTGGTCTGCAAGCCCTT
				---	TGGCAATGTGAGATTGATG
				---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGATGAGTGAAGATGTC[CT]GGCTCAG
EST19590	55	C	T---	---	GATGCCGGAAATGAC
				---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAAC[CT]JGGCTCATACCTTTATCTATAGCCTT
EST76136	39	C	T---	---	CCCTTAGGCTT
				---	TGAACACCTGTGTGTCGGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGGAGTTTGTGTCTGTGTG
				---	CAGTCCCCCGCGCACTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAGAC
				---	ATTTACCACTTGCCCATGTCCCTGGCCTGTTGTGCACA[CT]JCTCTGTGAAGACCCCAACCCCTGC
ESTD- SPTB	176	C	T---	---	CTCCCCACCAAGCCAGTTTCTTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTACCTAGAACGTTTGTTCACACTTTCTTCCAGTATGGATGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THPB	125 A	C	---	TGGGCTTCTCCCGGAGGGTAGACTTCTTACTTGGCTGTGATTTCOAAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACAGGATC/CJCTTCAT CCACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAAGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTTCACCCCAACAAGAAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGCAAAATCAATGTCTCTCCAGATTTCA/GTATCCCCCA GCAGTGCATCCATTGACACATAATATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTGATCCATTTTCAITTTGGCCATAGGTCCTATGGGGATGACA
ESTD-TYR	122 G	T	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTGTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG/CJATTAAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A	C	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTGTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG/CJATTAAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A	C	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/CJTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C	T	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/CJTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C	T	---	TTCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGGCCCAAGACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA/CJTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A	G	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCAC[AG]TGGCGGGATGGCGGGGAGTTC TGGTTGGCGCCACGGCTGGCCCTCGTTGTGAACGGTAGCCTTTCGGGTGCGATGCCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGGGTGCATGCCTGAGATGTAGATGGGOC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACACCTCTACGTCAAGCCTCAGCACCAGATGCTGTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCA[CG]TGTGTTGGTGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAAGAAAGGGCCATCCAAAG
ESTD- TNFα	152 A G ---	---	TTCTGCATCTCTGTGGAAGTTAGAAAGAAACAGACACAGACCTGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCT[AG]GAAATCGGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTCCCCAACTTCCAAATCCCCGCCCGCGGATGG
ESTD- TNFα	88 A ---	---	TTCTGCATCTCTGTGGAAGTTAGAAAGAAACAGACACAGACCTGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTCAAGCTCCAGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGAAATCGGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTCCAAATCCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAATTACAGGGTCACTGCTATGATGTTTGGAGCCAGTCAACCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGGGAGTTGGGCGAGTACGGGCTGCAGGCATACACT[AG]AAGTGAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACCTATTTGCCAGCCCCAGGACAGAGTGTATCCTTGAACCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[AG]GGGCTGGCTTATCAGCCTCCAGCCAGCCCTGGCTGCAGA CATAAATAGGCCCCGCAAGAGCTGGCTGTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGTCACCTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGGCCCCCATGGGGGGACGTGGAAAGCCACTTGAGCTTCTGGAGAGGACCTGA GGGACAAAGGTCAACTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAA[AG]TCTCTCTC CTTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTGGTAGTCCAGTGTGACTCATCCAATGATTTCTCCAGTGTCTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGAGGACGGACCTGTCCCAGCCAGATGATTTACCATTTCCACAGTGGT CCC[AG]TAAACATCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

-189-

ESTD- AT3aa	60 C T ---	---	---	AGACCTCAGTTTCTCTGTGTAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCTTAGCA CTGTGCCCTGTAGTCTGTATCAGGTAGAGGAGATGGACACAGGTGGAGAGAAATTTGAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	---	CGGTCTTCCATCCAGGTATTGTGCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTA[C/G]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	---	ACCTGGTGTGCTGGTGTGGTGAACCTGCTCTTGGCATTTGCCGGCCCTCTCGGGCCCGTGG TCCTCCTGGTGTGGGTAGTCTGGAGTCAACGGTCTCTT[AG/G]GTGAAGCTGGTCTGATGGCA ACCCTGGGAACGATGGTCCGCCAGGTGCGGATGGTCAACCGGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGGCCCTGCTGGCCAACTATGCTCTCAGA ACATACCTACCCTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG[AG/CAACCTGAAAA AGGCTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGAGGTTTACCTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGAACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G ---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGTCACCTT[CA/G]GGGTTCAGAGTGGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[C/TT]GGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAATGGCAAGATATACAAATTTTATTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	---	GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAATCCATCAAAAGTTAACTCTGGGCAGATGAAAGCTACCATCCTCTCATCATGAAAAAC TGGGAGGCCGGGCAT[AG/G]GTGCTCATGCCTGTAAATCCAGCATTTTGAAGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAACCAACCTGGCCCAACAT
EST12274 0	135 A G ---	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTTGGCTTCCAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATATCTTCCCTCCTAGGATGAGGTG[A/G]TAGTAATGACCGATGGGTGAGAACTGTTCTGTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	---	ATGCTAAGGGGATGGACATGAAAGGACCCCTGTGAGCCGATTTGCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAAGGCCAGGCACTGGGCTCCGAGGACTCAACCACTGCCOCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T	---	TTACATTTGGGATGTTCTTTTGGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGGCTTGGCTGCCTGTGTGGGATATTTGAAGAGATGCTTTGGCAGTCCCAATGCTCTAGAGATTTGCCAATGTTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTI/AGTCTTTAATCCATTTGATTTGATTCTGTGA
ESTD-FYR1	109 A G	---	CTTCGTGACGGGAGGTCAGTCTCCGCTCTTTTCATGGACATATGGATGATGCTGACCATTTTCCCCTGTGACAGTATGACAGCGCAGACTTGTCTACTATAGAGI/AGGGGAGCTGTGTGCACATAGCCCGCTCCCTCTGGAGCTGGAGCCACTGAGAACTAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCCTGCGAGATGTGCGI/AGJCGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGCCCGTAGGGGAAGCTGGGGGATCTAGGGGATGGGTGAGGAATGGGCGCAGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGAGGCGGTGGAGGAGACAGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G	---	GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTCAAGGAIC/TJGTCTGTCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGAGTGGG
EST12839 3	122 A G	---	CCITCTCATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAAI/AGTCTCTACCCGAGCTTGCTCGCATACAGACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGI/AGJTCAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACITGAATGTTATTCAAC
ESTD-ACE	96 C T	---	TGGATTTCCAGTAGGTTTCAGTTTACTTATGAATATTATGATACCTTAGCTTAG
EST54419 8	88 A G	---	ATGGCTTGCCTTGGATTTCAAGCGGCACAAGGCTCAGCTGAACCTGGCTI/AGJCCAGGACCTGGCCCTGCACCTCCTGTTTTTCTCTCTTCATCCCTGTCTTCTGCAAGCAATGCAAGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCGGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAGCCAC
		---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGAGTACAAGGATCTGCCI/TJGTCTCCCTGCGTGGGGGGCCAAACCCCGGCTTCCA
		---	TGAGGCCATTGGGGAGCTGTCTGGCGCTCTCGGTCTCCACTCCTGAACATCTGCACAAATCGGCGCTGCCTTCGCTAAATTTGAATGATATTGTGTGTGGGACCTGAGCAGCTTTATGGCACAAATGATCACTA
		---	TTTTCTTGACCCCTACTTACI/AGJATCCTGGGAGATGATTTGGGTTTAGCGTGGTGGTATGTTGTGCTACTATAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---	---	---	GGGAGTAAACTTGGATTGGAGATTTCATTTTACAGTGTCTGGTTGGTAAAGCCCTCAGCAMCA GCCAGTGGAGACTGGAAACACACCATAGCCTAGJTTCGTAGCCATATTAAITGGTTTGTGGCTTAC ATTATTACTCCTTGGCAATTTTCAGAAAGCATGGCAGCTCTCCAATCTCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCCGTGGAGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGGTCACTGCTGGCCATGGCCCTGGAGCTCCGAGACTCCAGACCATTGACCAA CGTGTCTGTGACTTGGCTGGCCGAGCCGACCTGGTGTGGGACTCCTGGTGGCGCGCGCGGCGCA CCTGGGCG
WI-567b	48 A G ---	---	---	TCTCACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCCTGGTTCTAGAGCCCTCATCTCTTTA CAGGATCCGCCACAGATCCCACTGATCTGGCCTTAGGCTCTCTCTCCAAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAGGTGATTCTGATGCTACCATCTTCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTGTGTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGAGGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGMAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTGTGTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGAGGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAATTCACCTATACAAGAACTATTTCTCAATTAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTTACAAGTACCCCTTGTATTATTTTGTATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAAC/TTCTTAAGTCTGCTTCAAGTCAAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAAGATCAGTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-1008b	205 C G ---	---	---	TAAGGGCTGTCTTCCCCACAGGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATATAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGGTC/GIAGCAGAAAGCAGCAAGGAGGAGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGG CAG T C C T G G C T G A G T G G T A G A C A G C A C T G A A G G A T G G A G A G A G A A A A C A G G C A G A A G C A C T G T G G T A G T T A A C A A G G C T T A T T A G G A [G/A] C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A T T A C C A G C A G T G A C A G G T T A T C T G G T G A A T T C A G T A T T C C A C T T G C A G G A G A A A G C C A G C C A G C A A A G
WI-2924	54 G A T A G G	T G A C C T T C C T A G T C T T C T C T T A	G C C C T A A G T G T A A T C A C A G G G	T C T G T T G T C A T A T T C C C T C T T T G A C T G T G A C C T T C C T A G C T T C T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T T A G G C C T A C C T G G A T T A T T A G A C A A T C
WI-2939	72 G T G T G C C T T T	G G C T T G T C T C A G T G C C T T T	C T T G T T G A G G G A A G G T C T T G	C C A T T G T G A G G T G G G T G G G T C A C T T G T C A T T C C C T G C A C T C A A C A A A G T G G C T T G T C A G T G C C T T T [G/T] C A A G A C C T T C C C T C A A C A A G A A T G T C T T T C C A T G C T C C G G T T C T T T G A A A A T T C G A C T T T A T C C T G A A A A A C T A G C T G C A G T G T T A T C T C C G G T A T A A G C C A C T C C T G
WI-3203	99 G A A G A C G A G	G G T T A T G C G C G A C A G A G	T C A A G T A T T G C C T T G T G T G G	C T T G T A C C A T T C A C A G C A T A C A C C C T A G T G A A T G C C G T A A C C C C A T T A T A A A C A T C T T G C C A T C G A A G G G T T A T G C C G C A G A C G A G [G/A] C C A C A C A A G G C A A T A C T T G A A G T A C T T G G A G A A T A A G A T T T T G G A T G G A T G A A G C A G A G A G A T G C T A A A A G T G A
WI-3473	101 A G G C C T A G G G A	A A G C A T T T T A G C C C T A G G G A	C C T G A T G T C A C C A A C A T T T T C T	G G A A A G A A C C T G A A G G A T G A T A G A A G T T A A T T G G G A G A T A G T T G G T A T A G G C C C T G T T T G G A G A T T G C A G A G A A G G A A G C A T T T A G C C T A G G G A [G/T] A G A A A A T G T T G G T G A C A T C A G G G C T
WI-1796b	29 A G ---	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T T T A A G C A G G A G A C A T T G T C T T G G C T C C C C
WI-1796	29 A G ---	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T T T A A G C A G G A G A C A T T G T C T T G G C T C C C C
WI-4360	93 C T A A A T A A	G T A G T C A C A T T A G G T A T T T C C	G A G A G A T A T T T T T C A G A G G C A T T T T	A G T C G T C C A T C T T C A G G G T C T A A C T C T G G A T C T G C C C T G C A G A T A G G A A A A G A A G A T G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C T C T G A A A A A T A C T C C C A T G T C C C T G T C T A A T A T A C A T T T T C C C
WI-1959b	87 C T ---	---	---	G C T G A C T T T G T G C A G A G C C A G G G A C A A T T C A G T G C C G G A T T T A T A T A G A T T C T G C A G C A C T G C A A C A G G A C C A A A A T C A G T C [C/T] G G G T A A C T G A G A T G G T T T T C A C A C C C A A A
WI-1973b	28 A G ---	---	---	G T T G T C C C T G T A G C A G A C A G A G G C A [A/G] A G A G G A A A A A G C C T T T T T G T C C A G G G G C T T A C A C T G A A T C C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T A G A G G T A A T A C T A A G T G T G A G A A A A C A A A G G T A T A G G G T T T G
WI-1980b	140 C T ---	---	---	C T T G A T A T G C T G G A T T T T G G T A T A C A G A A A T G G G A G A G C T G G A C T A A T C C C C C C A T A T A C C A A G G G A C A A A T T G T A T C T G T T C T A C A A T T A C A G T A G G A G A C A T A T G T T C C A T G A C A A T G G T A A T T T T T A A [C/T] G A C A G T T T T A A T T G A G T G A A A T T A C C A T A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T T A C T A G G T G C C T A T A A A T A G C

WI-2015b	190 A G ---	---	TGTCAGATAGTCCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAAATACAAATTACTTTGCAGATAGCATGACCATGCTAGTAGAACCCCAAGAACTAT GTGTGAATCGTCTATTAGGGTTGCTATAAACTCTACATGGTGTCTTTTCCAACTGAGCATATACATCTT CTAATACCATAGAG
WI-754b	49 C T ---	---	GAAGGCACAGGGAGAGATGGCTGTCTATCTACAGCCAGGGAGAGAGAGCCTCTACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGTTATTACTTTAGA
WI-754	22 T C ---	---	GAAGGCACAGGGAGAGATGGCTGTCTATCTACAGCCAGGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGTTATTACTTTAGA
WIR-1b	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAAACTCTGATGATGATACATCCGAGJTGGCGTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAAACTCTGATGATGATACATCCGAGJTGGCGTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---	---	TAAATTTAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGTGA/GTCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---	---	TAAATTTAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGTGA/GTCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---	---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---	---	CGGCACAGAGACACAGAGAGAGAGTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---	---	CGGCACAGAGACACAGAGAGAGAGTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---	---	CGGCACAGAGACACAGAGAGAGAGTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCMGGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGGCTGTGGTCCCAGTGT AGGTTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A G	---	---	---	TAACCTGAAACTTGTCTCTCATCTCAGGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AC] CCGAGCTTGGGTTGGGCGAG
WIR-6	63 A C	---	---	---	TTGCTGACTATTCTAAGCATCTGTAGAATATTGAATACATAGCTTTGAGATTGATC
WIR-7	12 C T	---	---	---	GGCGTCTATGACTATCCTGGTCAATTGATTGACTAATGATTCCTGCTGGCCCTTG
WIR-8	46 C T	---	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAAGTTGTCAGAAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCACTGGCTTGATTACT GACAAC
WIR-2	56 C G	---	---	---	TGTCCTTGCTTATGCCTGCTCTTTGCGCTTGGCAGGATGCTGTCATTAGTATTTACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCATTOCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCAGTC
WI-7069	93 G A	---	---	---	GGTCATTTCCTTTTTATCTGTCAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T	---	---	---	CCTATATTTC AGTTTGGAAA
WI-18612	37 A G T G C	---	---	---	TTGATTTGCTG CTTGCAAAT
					CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]ATTTCGAAGCAGCAATACAAAAGTA TTGATGAAGAATGCATAATCTCTGAAAATTATGAAACATCCCT

WI-18517	87	C	T	CAGCCTGA	CAGGAATCAG	TGTTTGG/CAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTGTGTCAACTCTACAGCCCTGCATGCC ACAGGAATCAGCAGCCTGAG/CTGTGTGCACCTGTCCAAACACAACTG/CTGC
WI-18668	76	C	T	TAGGCAAAA	GGCGAAAAAC	GCTAAAATTAAA CTGCACITTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTACAGTCCAAATCAGGTAGATTGGCGAAAAACT AGGCAAAAAC/CTAGCAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCTACT
WI-18680	75	T	C	A	AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCACTCCCTGAGTCTGAGTGGCTGTCACTCTAGC ATCTGGAAT/CTGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGGTAC	GGGTCTCCGA	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGGAGCACCACACCAAGGCGAGTTGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC/CTCCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---	---	---	TGTGGGCAACCTTGTTTTAAATGGCAAC/AGTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	G333	GTCGTGGGGT	GCAATACCAC TGAAGAGGAC A	ACCAGTCACTTTTATTTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGTCTCAGGAGGGGCTCGGGCCAAAGTGTGGGGTGGGGGTGCAGAGT/CTGTGCTCTTC AGTGGTATTGCGGACC
WI-18533b	91	T	C	---	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTTTAAACTCCCGAGATTTCCTCTTTATT TATATTTCAITTTTCTCTAA/CTTACTAGGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCAATTTTTTAACTCCCGAGATTTC/CTTTA TTTTATTTTCAITTTTCTCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TTC	TCATCTGATAC CTTGTTCCAGAT	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCAAGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTTTTCATCTGATA CCTTGTTCCAGATTCTG/CAAAATAGTTGTAGCCTTATCTGTTTACAGATGTGAACCTTT
D49493	159	A	T	CTGCGGAATT	CCTGAAGGAA	ACTTTCAGGCC AGGGC	CAGGACTTGTGTGTCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCACAGAG AGCTGTCCGCGCAGTGCATCATTAGGGGGTCTTTTCACTGTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/ATGGCCCTGGCCTGAAAGTGGCCCATCATCCACTGTT
EST10030	7	98	T	CTCTCAAGTCCC	CATTCTGTTTC	GCAGTGGTGGT ATGGATGA	CT TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT/CTCATCCATACCACCTGCTGATTG
EST10052	2	24	G	A	GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCAGTCTGAGGAGGCTG/AAAGTCTAAGATTGAGGTTCCACATCTTTGTGAGGGCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCACTCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA

EST10605	118 CG				CTCTCAAGTAG	GCTAAATTTC	CTTGGTAAATCACAGTTCTGTATTATCATACAAAAACTTTTGTCTCTGACAAAACGTACACATAGA
2					ATAAGAGGCA	AGAAAGAATT	AAACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCATGTCTGTTGTGAGACTTAA
EST11048	61 TG				TAACT	TGTTT	AAAAAGAAAAAGATCCC
0							CATGTGTCATCCCATGATTGTAAGAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA
EST11260	101 GT						ACAAATTTCTTTCTGAAAATTTAGCTTATGAACCTCAITACACTGCAAAACCAGAGAGGAGCAC
8							TATGGAGGCCAGAGGAAGTGACACTATAITGTGGAAGTGTCTGAAAGAAATGAAGTGTCAACACAAWA
							TTCTATATCCAGCTAAATATCATATTAAGAATGAAGGTGGAAATGAAGGCAATATCAGATAAA
EST11349	109 CT						TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACAGTAGATTCTTTGGACGMAAGAAATCCT
9							TCTGTGGATTGAGCTTTACCGCTTTCTCTCATCTGCTGGTGTCTTCTCTCAGAGCTTTAATGTCCGT
							CCGTCTCCGAGTCAG
WI-16632a	71 AG				CCAACCTACTT	CTAAAACTCC	GAATCTGGGTATTAAATAGCGGGTGCCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG
					TGGAGCCCT	T	CCCTI/AGJAGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA
							AAGGGAGGAAGGAGTGGGA
EST11772	74 AG						CCAGGAATAAAGAAAAAGAGTCAGAGGAAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC
6							TTCTTCA/AG/GACTATTTCAATTTGACTATAAGTGATAAATACATTGAAGACTTCAGGAGCTCA
EST11795	82 GA						CTTGCCATTTATTTGTGCATGTGTTCTTAAAGGCTGTGTGAAAGATACTTGGAAATGTGGGAAAC
3							ACATAGATCCCAG/AG/ATTAAGGGGCTGGAAAAAGT/AGCTTAAAG
					CAATAAGCAG	ACTTCATGAAT	AGAGCAATGGTCGATCTCAATAAGCAGCTATTTTGATTAAC/AG/AGGTATACATGAAGTAAATTC
					CTCATTTTGAT	TTTACTTTCATG	ATGAAGTAAATTCATTATACCAAAAAGCCCTCCACAGAACTTCATGCACCTTGAGCTATGTGAAC
WI-16644	42 GA				TAC	TATACC	TGAAAGTAACAGTGGGAT
					TTGTATAATA		
EST12005	56 AG				ACACTCAGTA	GGCTGGTCACT	GCCTAGTAATTCAAAAAGGAACATGTTTGTATAATAACACTCAGTACAAAAGTCTGT/AGJATCCAGG
9					CAAAGTCTGT	TOCTGGAT	AAGTGACCAGCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTCCTCATAGTTTTTGAATC
EST12055	32 TC						GTGGAATAATTTTTTATCTGTACGCTTTTCCT/CT/ATTTATATTATCTTGCTCTTGATTTAGCACCC
9							CACCCGATTTGCAGGCAGTGTCTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTCT
EST12492	95 AG						CCCTAGCAATGACTTGGAGTTGTGTCCAAATACCAGTTACATACTGTTGCCAAAAATTAAGCTCTC
1b							TTCCAGAGGCATTAACTGAGATTAT/AG/GGAAACGCCACAGCAAAATGACCGATGCAGCTTTT
							CCTTTTA
EST12492	25 AG						ATCTTGAGGTTTTCTGGGCTGTCA/AG/AGGTGACATCTTTTACTTAAACAGGTGAGGAACCCCTAT
4							AAAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAACCAACTGGAGGCAAGTCCACAGGTCACACTGTCAIC/G/CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCAGGGGGAATGACCAATTTTAAAGGCCATGTG GTGCTCGAGGCGATTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAAATTAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTTCAATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCACCCGGC/A /GTTGAGAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCGGAAATTCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATTCAG/C/ACTGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGATGGGAATCCATGTTGCTTGGGTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA/T/CAACAGCCAGTATTTCAACCAGAAATTTGTTGGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC/A/GTCTGTCACTTG CAGAGACCCACAGGAGACACATTCCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA/C/TGGAGCAGAAGCAGCTTCCCACCCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAAATTGACACCAATAAATGCAC/A /GTATTTAAAGTTTACAATTTGAGAAAGCTGACAGGTGTCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC/C/TJAGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGAGGCCAGTCTCCTCACTGTCCTCATGAATAGCC AGCTTATTCTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAAATTAATGAAATAGTCT GGCCATT/T/G/GACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTGCGCGTCAATATGCAGCTCAGATGTGAGAG ACCG/GAT/CTCTGTACAGGAGCGGTACTGTCTTCAATCTTTCATGTCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CC/T/C/TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGATATAACCA

EST13278 2a	51 A G G	CTTACCGAA CAATATTTAG G	CATATCTGG GTGGTGAGAA	TTGCGAAGACGTTTACAGCTCCAAACCTTTACCGAACAATATTTTAGG[A/G]ATTTGAAATATAT TTCTGTAGTTCTACCAACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	AGTCCAAGA	CCACACATTTG GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCATTTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGGTGAATTAAGCC TGCCTGAGAATCCCAACACATTTGAGTCCAAG[A/T]AACCTTCCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G CTT	CAATTTTGA AGTTGGGTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTTGGGCTTTTGG
EST13518 2	45 C G	---	---	GAAACATCCTCCAGTAGTATTGAGGTAAATGATTCAGCATTTA[C/G]ACTTTTAAATTAACCTCA ATGTTCCTCGGAGTCGTCATAGTTTAAATGACTTCTGACCTTCCTTATAACCTTGATTG
EST13522 8a	66 A G	---	---	CAGGTTGGTGAATCTCAACTAGGAGCTATTTGCCCCCATCCCCACCGGCGAGTGTCTGGAGAC[A/ G]GTTTATTGTCACAACCTGCGAGAGGTGGTCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G	---	---	AAGATTACGGACCATAAAGAACTGCCCCCGACCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAATAAGTAATGACTTCTTGAACAA[A/C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G	---	---	CCTCAACCATCTGTAACCCGAGCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G	---	---	CAATGGTGTCCTCATGTGAACATAT[A/G]ACCTATTTCATAAAGTTAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGAACGACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTTGGCATGCTAGACAGAGGGATTAT[C]TTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCTTCACACTCATTTTAAATTTG
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TAATGACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAATCTTTAGAGTCCCGGAGTTTGCCCTTTTCTAACAATTTTCATATCAGGTGAAAAAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCCACG ATACTGGTT	CGGGAANAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCTCCCACTGAACCAAGTAAT TCACACAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAATACCCCACTACTGGTT[A/T]TTCC GGTACTGTTTTCGGTA

EST15420 6	109	C A	---			TTTAAACCCCAAGACTGTAGATGTCAGGACCTCGATCATTTTCTCTGCTATAGCTTGGATATCTTA ATCTCTCCGCTTTGTCATCATATAATCATATAGCCAAAGGACTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48	G C	GGA	GAATAGCTGA AACAGAGATA TTATTCTC	GAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAGACGTGAAAGACAAAGACAAAGAGAG/GC/JAGCAGAGAATAATA TCCTCTGTTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57	G A	CACAAGC	GGTTTGCCAT CTATAA	GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCAACAGC/GAJTTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAATGGCTCCCAAGGT
WI-16782	96	C T	CACGTGTAAGG	GGTGGAGTCT TC	CTTCTATCTTT CTGTCTCTCCA TC	CTTCTCTCTCTAGACGTGGAATACACACGAGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATATGTTGGGAGTCTCACTGTAAAGG/C/JGATGGAGGAACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTTGGGG
WI-16783	64	A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G	CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAACCTTAGAGGTGGCTCTTTTGTGTCACTTTTCTGTGAGATGCTTTTACCTGAG/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACCTGAGT
EST15948 2	58	T C	---			CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTAACTAAAGGTCAGGGCAACATAGGAT/CJGTGA CAGCACCACTCGGACCAAGGAGTCTGAAATCGTCACACTAGCGTGGCCAGCCCTTTTCTCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89	G C	---			GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGATTCATTTTGTGAGCTGTTTGTGAGCC TTTTCCAGAAAGGCCGCTC/GC/JGGGTTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96	C T	---			CGTCTGAAGTTTTCTTTATCACAAGTCAATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/JAAGAGGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24	C G	---			ATCCCAGCTGTGAAGGGACAGGAG/C/GJGTAACACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGTCCAAATAATGCAACATTTTTCACCTCGTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83	A G	---			TTCCTTTAAATAACCCACAGACACCCCATGACACTTCCAATTTACAGAGCAAAAGATTTGCAG CTGGTTCTCCAGGGA/JGJTTGGCCCCGAGGCTGGCTCAGTTACCTCCAGGACCTCAGTC
EST16118 0b	119	T C	---			ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAAATGATCCCTTTGGCTTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32	C G	---			ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAAATGATCCCTTTGGCTTTCCCGTGGC ATGCTCTTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 CT ---			AGCCAAITCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATTAC/TAATGAACGT AAATAATCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 GA ---			CATTGTTGGGTAGGGAAAGATAGTAGTGCAATAAAATGGTAAACAGCAG(G/A)AAATGGAA TTATAGCTTTCTTTTCATATAGGGAAATTGAAATTTATTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 AG ---			GCAGGTAACACTGGTTCACAACTGTTCTTCATATAAAGAAAGAAATATCTAGTTG(A/G)GTAG AGGAAGGCACTGCTCTCCGCGCTCTCGTTTCATATTTTATGTCACGTGCTCCTAACGTGGGCCGTGT GCAAGAGATCTTGAGA
EST16198 4a	28 GA ---			AATCTTAGGCTCTTGGCTTTCAAATCA(G/A)ACAGACAGATAAGAGCTTTAAGTATTTGCGCATTT CCCCAGAGGAAAGAGTCAGCATCAAAACACATGGTCCATGCTCAGGCACATGGTGTC
EST16229 2c	52 TC ---			TGTGAACCTCGAATTGGCTTGTCCAAGTCCCTGAGTCACAGTTTCATTTGGGAG(T/C)CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCAGTAGCTGATTACAGACAGGAGGCTGCA
EST16229 2b	45 TC ---			TGTGAACCTCGAATTGGCTTGTCCAAGTCCCTGAGTCACAGTTTCATTTGTTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCAGTAGCTGATTACAGACAGGAGGCTGCA
WI-16816	124 AG TGGGTTA	GGAGCCATTGT GCTTAGATTTT GTTCAGGACAG		CAGACTTTTCCCTCACACCTCATTGGCTGGAACTGGGTACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTACATAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA(A/G)ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 GA ---			GCCACTCTCCTGTGGCTTGTCTCTGTCAGGTGCTGCCAGTGCCACAG(A/T)GGTGTAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGGTGTGCTGCCACTCTCTCTCTTCCGCCGCTGGGCTCACCACC TCTTCTCCTCAATC
WI- 16824b	83 GA ---			GTCACCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG(G/A)CTTACACCTTTAGCACGGATAGTTTCTGTTGCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI- 16824a	47 TC CAGCTGT	TGATGGTGTG TTCTTCATAAG AA	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTGTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGTTACACCTTTAGCACGGATAGTTTCTGTTGCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 TC ---			TTGCTTTTATTAAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTCATTACAAA AATGGCTTCCAAACCATTTAAATGAAC(T/C)GGAAATAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACAAAAAAGCAGTAATGGCAAT(G/A)CTAGTGGTCTTCCCAA TTCAAGACCTGTGCTTCAAATTTTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C	T	GATACAGGCC ATAATTTCCCA CC	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99	A	G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAAATCTCCCCCTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC/GJGCGATTACCTGACATGTCATCTCCCT
WI-16888	70	G	A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/GA/JTTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA/C/JCCCACTGGCTAGAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTCTTAAGGAGGTTATATCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAM/GA/JGTATCTGTTATAGAAACGATACITTCATTTTGGGCTGAACCCAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA TACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATCTCTCTGTACCCACAGACACTAAATCTAGGAAATTTGAC TTTACTGCAGGCCATTAAACACCAGCAC/C/JGATGCCACTTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGG	ATGTGATTGCC OGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCCCTGGAGCACAGGATT TGGCTGAGGCTTCACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/C/JCCA CGGGCAATCAGATGAGATG
WI-16947a	58	C	G	CATGGAATA GGCCTGGAG ATCCTGT	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCCCTGGAG/C/JACAGG ATTTGGCTGAGGCTTCACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAACAACCTAAT/C/JCTTAACTTGGTCCAACTATTT AGTATACTAATATGAGTTTTTACTGATAACTTGCAATGCCATTAA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATTT/C/JACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTGAGCTGAGAGGCTGAGGTGAGTCAATCT
WI-16992b	60	T	G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTGCGCCCTCATCTGAGAT/GJGTG TAGGACTGTAAAGGAATGTGTTTGGGGGTTAGGAA
WI-16992a	46	G	A	AAGCAACCAG AAGTACACTG TC	CACATTCCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTG/C/JCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA AAAGCCATG CA	AATAACGGT GTTTGAATGT CA	ATGTTTCACAGGAAAGCCATGTCATGACATTCAAACACCCGTTATTATTAGAAGCTCATTTAAT TGTTTAATGCAGACAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C T	CACTCGGCAC TACACAGAGT	GGGAGGCGAGG GGTG	ATTCGGTCTCCTCAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCCTGGAGCCATGGGGCACCCTGCCCTCCCCAGGCTTCTAAGTAAACAACT
WI-17040	94 T C A	AATTCCTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGGCTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCGAGTTC GAGAACTCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTCC AATCTTCTCATATGT
WI-17044	47 G T G	GCCAAGGGAT TAACGTATAG	GGGATCCCT TGTTTAAGA	TTGTTTGTGTTTCTCTCTCTGCTGCTGCAAGGGATTAACTAGGTCGTTCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAAATGGCAGGAATCGAAT CAAAAGAAAGCAAGTG
WI-17021	62 T A ACTC	TGGACTTGTC GCCTATACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCTATAACTACTCTTAAG CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTATACAGGAGCAGCATGCCAAAGTGCCTGG GAGTGCCCAATAAATCAA
WI-17065	90 T C CTT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAANAATGTAGACATGGGGAAAAAACAATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTTTCAGGATTTCATGTCTCTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTATAAGGTTGTACAGCCAACATCACTGTTTTCATTCAGAACATTTTCAACATCTCAAAAAGA AACTGCAACCCATTAGCAGTCATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G ---		---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAGCAT AACCTCCTACACAGGCCCTTTCATACATAGGAGTATATTTGGCCAAAGACTCACCACCTAGAAAGTATT
WI-17104b	108 T C ---		---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTCGAGCTTCCCATTCATCCCA AATCAGAAAGCAGTCAGTGGCCCCGTGGTTCCAGAGCGGCTTTCCTCTTTGTTAAGAAATTA
WI-17114a	37 T C GACTTTGTTTT	TTCCATCAAG GACTTTGTTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGAGATGTTCCATCAAGGACTTGTGTTTTCGTCCTTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAGACTGCAGCCACAATCAGAGTTACAT CGGA
WI-17150	76 T G CTTT	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCCTCTTTCATATCTCCAGGATTCTGAGAAAGGCCCTCTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT	CATTCTTTGT AAAATAACAA	CAGAACTCTGC TTTTGCCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAATAACAATAACGTTTTCAGGCAAAAGGCAAGATTCTG TAACCAACATTTGAAAGGGGACACAGGAGGGGCGAGGGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAA

WI-17178	127 T	C	GGACTCCCTCA	CCCTCAATTT	AGCAATGTCCCTCCAAATTCATTAGCTATGATGGAGTTATCAGTTTCAGTTTCAGAGGAAATTCAGG
			CGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAATATCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180b	81 C	G	GCAGTTGAAATTGAGGG
			CACAAAATA	...	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCCAAAGTCCTGCGCACAG
WI-17180a	47 T	C	TGCA	TGGACGAGAC	GGAGTC
			TGTTCTTAA	TGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCCAAAGTCCTGCGCA
WI-17156	54 G	C	TCCA	CAAGAAATAT	GGAGTC
			CTTTAGATATC	ATATTTGATTC	CAGGCTTCAACAAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17149b	79 T	C
WI-17149a	48 C	G	AGGAGGAACA	CATGA	TAATATCTTG
			CAAGTTTGA	CCACGACGTG	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAACTTTAGATATCTCCCATTCCTCCACAGA
			GCAGAAGTAG	GGTGAGGTGGT	ATCAATATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
WI-17197	67 G	A	CTGGGCTAC	GCATACC	ACCCTTCTG
			TAATATCTTG
WI-17198	38 A	C	CTAGTT	ACTGAGAAAT	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGACGTGCGTGGAA
EST18753	27 C	T	GGTCTCAT	GGATCGCATGA	ACCCAAATTTGTCATTCGTTGATGAACACTACAAAAGGATGGGAAAGAACACATTTCTCTCACA
		
WI-17108b	74 C	T	CA	CC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATTCCTCCACAGTGGCGTG
EST19067	41 A	G	GAACCCCAATTTGTCATGTGTATGAATACACAGATAATGCAAGATATCTTACAAGAAACAATGCACATCC
			CGTGACCATTT	AAAAGTTGAA	ATTTTGTCTATGTTGCCCTGGGCTGGACTCCAGCAATCTCTGCTGCCTCATCGGATCCCTGCTGCTGAGTGGCTGG
EST19067	40 A	C	TTC	CCA	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATCGGATCCCTGCTGCTGCTGAGTGGCTGG
			GATAAGACAACTGCCACAGGCCCTGCCCTAGGAGTAGTCTTAATGCCGTGATGGTGGG
EST19125	28 A	G	TTATTTTAAACATAAACCAGATGCACTGGTTTGTATTTTACATTTCTGTTGCCATTCAGTCTCAAAGT
			AAACACATCTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
			ACACAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JG/JGTGGCATTAAAGTACATTCAACT
			TTTGGCAACCCGCCATCACCATTTCATCTCCGTT
EST19067	40 A	C	TTC	CCA	ACACAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JG/JGTGGCATTAAAGTACATTCAACT
			TTTGGCAACCCGCCATCACCATTTCATCTCCGTT
EST19125	28 A	G	ACACAAATTTACCATCGTGACCAATTAAGGGTATAGTTCA/JG/JGTGGCATTAAAGTACATTCAACT
			TTTGGCAACCCGCCATCACCATTTCATCTCCGTT
			CTGTTTCTCAGAGATGACACTGCCAACA/JG/JTCACAGATTTGCATACAAATACAGTTATGTATTTGGC
			TATTCACAAATTTACAGTAGTGTCTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGAGT TGGACCGA	AAGATTTTATC TGGACCGA	GTGTGGAGCCGGAGTTTATTATTATTCAAATCAGTCTCTGTGAAAACCTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTCGGGGTCCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTCCTA	TTGGTTAATGATGCCAGATGGGTGCATCTCAGAACTTCTCAGCCTAGGCTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGAGTGGGACCA
EST21904 b	128 G A G G	TTATATGGCC ATTTTAATAA	GGCAGGTGTC AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTTTCGGGGCTGTTTCCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTGCCATTCACCGCATCTCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAAAATCCACCACCTGTAAACAG TAGCATCAATGGTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATCAATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT	TGAATGCTAC TGTTTACAGTG	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATTCGTCATATAATTCGTCATATAATTCAGAA CAGTAGCATCAATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC[A/C]ACCAAGGGACGTGTGTCCTCCAGGGCCACCGTCGAGGCAAGTGTG GTCCAACTCCTCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCTTCT TAAGCCTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAATTT CTGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAAATGACTTAAAAATAACAATTTCTATCCAGAAAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T	ATCCTTTTGT	TTGCTGTAA	TTTGAAGTAA	GCCTTTTATGTCTCTTTTAAACATCAAAATGTTTATAACACACTTGATCTCTTTTGTCTACCCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATTT
EST23021 0	108 T A	---	---	---	TTATTTCTCAGCTTACCAATTTGTTGTTACTATCTCTGTACAAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTAAATCTTTGCCCTT/C/ATGGGTTTTGACAGTTTGTGCTTTCT
WI-17387	55 C G	CCTTTGCAGAT	GCCTTTGCCTA	AGATTAATAGT	ACAGAAATTTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT	CCTTCCCTCC	IGTAAGC	TTTTTGGCTTGTCTGCAGATAGATGAAAAAGAGAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTAGTT	TGCACCTTAA	TCCCATCAAT	AAAGCTGTAGTTTGTGTTTTTGTCTTTTCTT/C/GTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAAGGCTAGAGAAAGATATAGGCCCGAGAGAGGCTCAGAGATTTCTAGAGCGGCGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCGTOCCG	CCAGTGACGAG	GOOGA	CTGACAGTCCCTGTGTGGGGGTGCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCC GTCCGCCAGCCCT/AGTGGCCCTCGTCACTGGCCTTGGTCACTTTGTATTTCTGCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC	AATTATTAT	TGCAGGCAATA	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAAATGAATGCAT/C/JAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAACTTAGAACAGTACATGGTGCAATAG
EST25356 3b	95 C G	---	---	---	TCCTTGATACAGGTAACCAAGTTTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	---	TCCTTGATACAGGTAACCAAGTTTTGT/C/JACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	---	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGAGAGAGATTGGATCCAGCTTCATTCAACATT ACTACCAAGTTATTTGATAATGATAGAACCCAA/C/JTAGGGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT	CGTCAATGTAA	ATTGCGCCT	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGAGAGAGATTGGATCCAGCTTCATTCAACATT ACTACCAAGTTATTTGATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCTTGTG	CAATCTTATAG	CTAGAAATCGA	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGGCGCTACT TCCCTGTGTAAACACTCCC/AGJATATTGTGCTATTTCTAGCTATAAGAAATGGGGCCACTAAGTGGGCTC

WI-17623	46 T C ...	---	TG TGG TTTTAA TTTTCC ATATAA TTAATG TGTGGG CACATTC/CJG CATGTGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ...	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/CJGGGCAGTCCAAACTTCT TGGGAGGAAGTAATTCATGTGTAATGTCATGATGGCTGCTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG/CJAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAATTCATGTGTAATGTCATGATGGCTGCTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ...	---	TCAGCTTTAATTTAAGGACATGTAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/GCJAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTCTGCTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26900 7	39 A G ...	---	TACTTCAGTTTAAGGCAAAATTCACACAGAGACTGTCTCJA/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ...	---	CAAGGATTTTATTTTGTCCCTAAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/TCTCACATGGTGTACTCTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTGTCACTTTGCAACAATTTAATAATTATC/GJA/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTCTGTACACATTTCTGTTAACAAAGAACCCATACATT GGTAAATTCATTTCT
EST27662 4	51 C T CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCCAGTCTTG/CJTAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTITAGGAATGTTT
EST27788 3	100 A G ...	---	ATTTTATTAGCGGTACAAATTCCAAGGTGTAAGGTTGAAAGGAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACCTTACATTCAAGGAC/JGJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC C	GTGCAAGAGAGG TACTCCAAGTA C	TCCTCTAAAACTTTCTTCTGTTGGATCCCAAGTACGTTGGAAGTCATCAGAACCCCAQ/GJA/GTACTT GGAGTACCTCTCTGCACCAAGATAGTGGCTGATTTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAACAATAAATTTCAATCTGTACACAATC/GJA/JAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ...	---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/T/CJAAAAAGATGATCAATCTGTGGCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACCGCTGCTGAAGGAGACTGCTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31	T A	GGAGTAAAG GTGTTCTTCT TTAA	TTTCTGCAAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAATAAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50	T C	TGGGCTTCC TGTC	TGGTTGGCAG TGTC	AGAAITGGTCTAGTATCGTTACAGATTCGGTGATGGGCTCCCTGCTGCT/CJGGACACTGCCAAACC CACAGCTGGAGGGGACCTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68	T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATAGTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTCA
WI-17730a	39	A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTCA
EST29041 5b	53	G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTTGTCACCT/GA/GCTAACTCCT CAAATCAACAATACCCCTTTATTTAGCCATGAAAAAC
EST29128 4	58	A G	---	---	CTTTAGAGGACACCAGTCTGTTGGACTTAGGGCTACCCCTATTCACGAGGTGCC/A/GJTATTT TCACITGGTTACGTCGTAAAGGACCGTTTCCAAATGAGGTTACAGTACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATAGTGAACAGACACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGAAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	---	---	TATTTGTTGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99	A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTTACACTCTAAGTTATTTTAAATATCC/A/GJGGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86	G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAAGACCCAGA GTTTCACAAATATAGGTAGTGC/GA/JATAACACAGGCTCTACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAAGACCCAGA AGAGTTTCACAATATAGGTAGGATAACACAGGTTCTACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30	G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGCTTCTG/GA/JGCTGTTTCTTATACCCCAATATCATAGAATT GTTGTGCTTCTATATGTTTCAGCTTCAAAATCTTTTGTGTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

EST31951 4	87 C T	GGGTTGTCCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGTTGTCCAGCCAACA[C/T]GGAGGTGATTTTGGTGGGAATTCCTATCATCAATATTCT
EST31968 8b	95 T G	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCTAAAGATTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGGATTTCTGCTT/GA/AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75 T C	GCGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCTAAAGATTGGGGGGGGTTACTATAAGT GCATTTT/GA/ATAATGGGATTTTCTGCTTAAGTCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST32063 2	103 C T	TCCATGGATGAACAGACGCTACCATGCCACATCCCACATCCCTCCGACCAGATGTCTGGCCAGAGC TGGCTTCCCCCTCCAGACCTAGCTGGCTTGTAGT[C/T]GTTCCAGGCCCATTTGAATAGCAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	AAGGCTTTCCAAAGCATCAAAAGGCACCTGGGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCC[A/G] TCTGTATTAGGGAGCACCCCAAGCCCAAGTAACAATATGGTTCTTGCAG
WI-17800	29 C G	GAGAACTCA TT	TTTCCACAA TAATCCCAGTC	TGGACATGGGAGCACAGAGAAACCTCAGT[C/G]AAGACTGGGATTAAATTGTAGGAATATTTACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCATAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT[G/A]TTCTACATCAAGTAGAACCTAAGCCAA TCAGAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCAATCT
WI-17860	121 T A	TTTCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTAICTGATGTAGTTAACCATGGCCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAATCTTTA TAGTGCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAGCAAAATAT[A/CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA	CAGCAACCTTTTGTGTTTATAGCCTACTCTCAAAAATGTTT[A/T]TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAATACCA
EST33301 4c	80 G A	GAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACAAAGCATGATC AATGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A	GAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACAAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44 G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]TTGTAACAATGCAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC GG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACACAGTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACATA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TGA/GIGATTTTATTAGTTGTCTCGCTAGTAGTTTGGTATTCATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	GGACCATATG ATATATAACT CCTAAAGC	---	TGGGAAACACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAACCTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTTAAATGGAAGGAACCAACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTTAAAGC/C/TJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17993	118 A C	GTAGAGGCGA AGGGAACAG	---	CTCAGTAACCTCCGGTGATAATCTGCCATTTATTGATTTATGATAAAACAACTCTCATTTGTGA AAAACAGCTAAGGTGACATCTCCAGACCCCAACCACTGTCCTGTAATGTA/CJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGAGCATGAAACAACATCTCCCAGGCCCTCGCAGT AGAGCGAAGGGAACAGAG/GJCTGCCCATGTGCCCTGTCTCTAAAGAGCCACCCCTCAGGTTGATGT CACTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCCTTTATAAAACACCAGTCTCCCTAAATGT/C/GJATTAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTCC/C/CJGTTCTTAACCTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC CXXX	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC/CAG/JCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCTTGTTAGGTGCTTCTGTGACATTTCTCTTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTCATGTACGAATC/CJTGTTACACATCTT A/GJACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTAATGTCGTATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTCATGTACGAATC/CJTGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTAATGTCGTATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGGG GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA/GAJTGGAAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTTGTAGCAACAGAGGTAATG

WI-18064	54 GA	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/GAATGTAC AATCATACCACCTGGGGAGAAAGAGTAGACACAGTCTTATTTAGGTGCCAAACTGGGTACCTGGGAG GCAGAA
EST35347 2	97 T CA	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C GTGAT	AACCCACTAC TTACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTAT/CJATATTTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTTCTGTACTCAGAAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTTTTGTAAATTTAAATCTACTATGCCGTG TTTGACTTTTATCTCTTCTTATGTAAATGAAGCCAAATGCAITGTTAATCTCTCTCTCTTTGGTGTAT
WI-18080b	65 GA	---	---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTTTTGTAAATTTAAATCTACTATGCC/G/ ATGTTTGACTTTTATCTCTTATGTAATGAAGCCAAATGCATGTTAATCTCTCTCTTTGGTGTAT
WI-18080a	41 T C AGTCTCTC	GCAATATCA ATATCAAAT GTCAAACA	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCT/CJTTGTAAATTTAAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAATGAAGCCAAATGCATGTTAATCTCTCTCTTTGGTGTAT GTGGCATCCTATAAAAGCAGCCATGTGTTGAACAAATGATATGCACAGAAAGCATCTTCT/GA/ TGGCTTTGTACACGGTTTCTTCAAGAGGAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63 GA	---	---	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATTCCT TTC/CJTTTGGTATGAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115b	71 C T	TTAGTGACCT TTGGTATTCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATTCCT TTC/CJTTTGGTATGAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T TT	---	---	TTTGTAGAAGCAGCTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTCTCTTTA GGTAAATTGCA/GJTAAGAACAATAAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAAACT
WI-18136	78 A G	---	---	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGCTTTCCACTATGAAGGCAATGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC/GJGTGGAGCAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18169	115 A G GAAGTC	CCATCTTCCG	GAGTTCTGCTT GTGCTCCA	TGAAAGAAGTCGACACAGCGGACACT/GA/JTCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA
WI-18190b	26 GA	---	---	---

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGAG/GA/CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T	CAGA	AAATCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACGTCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT/C/CTCATTGAGGCTCCATAGGCTGCAAAACACATCAAAGGCATTAC TGTAAGGAGGACTGAG
WI-18327	104	GA	TT	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAAGGATTTTATTACCTACAACAAGTAAGGAGACAGCTGGGCAGTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTCGTTAGGCTAGTT/GA/AGCTGAGCCATTGTATGGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGAAAGCAGCAGCTAAACACACTCAATTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACG/GA/TTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	CT	---	---	---	GTGGAAAGCAGCAGCTAAACACACTCAATTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG TGGCTGCAGTCCTCTGCCGTGCTTGGCTCTCTGGACGTTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	CG	GCATCA	CCAGCCCTTA GCATCA	AAGGACTCAA AGACTGAAGAT GA	GTGGAAAGCAGCAGCTAAACACACTCAATTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG TAATCCAGCCCTTAGCATCA/C/G/TCATCTCAGCTTTGAGTCTTCCAGCCCCAGGTCCTCAAGCTT GTGACACAGACAAAGCC
WI-18012g	117	AG	---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTCCAGACTTGGAAAG ATCCCCGCTGCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCTG/GA/G/GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012h	113	GA	---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTCCAGACTTGGAAAG ATCCCCGCTGCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCTG/GA/G/GTGAAAGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCTT	GCCACTTTTC CCCTT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTCCAGACTTGGAAAG ATCCCCGCTGCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCTG/GA/G/GTGAAAGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTCCAGACTTGGAAAG AGATCCCCGCTGCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCTG/GA/G/GTGAAAGTTTCTCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	AG	CTCTGCATTG	GCAAAAAGGA CTGATTAAATA	GCTAAAGTCAG CTGATTAAATA ACTTAA	CATATCATAGCCAGATCTACAACCCACAGAT/ATTTCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG/GA/G/ATTAAGTTTATTAATCAGCTGACITTAGCATTTGGGAGATTATCTGGAT

EST38878 9	47	T C A T C T A A	A A C A T C A T T A C T A G C C T A G	C C T T C A A T A A A T C T C A T G T C C T C A	C C A T G A G A C C A A G T A A T T A A C A C A T C A T T A C T A G C C T A G A T C C T A A T T C J T G A G G A C A T G A G A T T T A T T G A G G G A A T C C T C A A T T A A T A T G A C A T T C T T G A G A A T G G G A A A T T G A A A C A C A T T C C C T T A T C A A T G T C A T C T C A C A C A T T C T T A T T T A T T G T T T C A C T T T C T C A A A T A T C G G A T T G T T G C T C A T G A G A A T A A T G G C T G A G G G A G C T G G C A C G G C A G T C T C T C A G C J G C T C C C T G G A T A G C T A A A T T T A
EST38882 6b	113	G C	T T A T C A A T G T C A T C T C A C A C A T C T T A T T T A T T A T T C J T T G T T T C A C T T T C A A A T A T C G G A T T G T T G C T C A T G A G A A T A A T G G C T G A G G G A G C T G G C A C G G C A G T C T C T C A G G C T C C C T G G A T A G C T A A A T T T A
EST38882 6a	35	T C T T T	T G C A T C T C A C A C A T T C T T A T	C G A T A T T G A G A A A G T G A A A A C A A	
EST38909 5	47	A G G C T A A A C G	G C A C A G C A T G G C T A A A C G	G G T A T T T G T G A T T C C A T C T T T	G C A C T A A A C T A A C T T C A T T T G G A T T G C A C A G C A T G G C T A A A A C G A G J A A A G A T G G G A A T C A A C A A T A C C A T T G A A G A T A T G G A G C A A G A G A M A C T C T C A C A T A C T G C T G G A G G A A T A T A A A T T
EST38911 9	85	A G C A C	G T T G A G G G A A A C T T A T A A C C T	T G T T G T T T G T G A A A C A A G C G	A A C T G A A T G G C A G T G A A A A C A C T A C A C A T C A A A C T T A G G G A A A T G T G T T A G T G T G G T A C G T T G A G G G A A C T T A T A A C C T C A C A G J C G C T T G T T T C A C A A A A C A C A G C A G A C A C A G A G A T T T C C A A C T C C A G C A A T G A C A G G C T A G G G
EST38955 5	30	G C G G T G G	T G A A T T C C C T T G G T G G	C A C T G C A A T C T C A C C C C C	T A A C A T T C C C A T T G A A T T C C C T T G T G G G G G G C J G C J G G G G G G G G T G A G A T T G C A G T G C T C A A G A T A A A T A T C A C A A T A T A T C A A A A C T T C A A A T T G T C T A T G C A T T C A C A C A C A T G A C A T G A G C C A C A A A C A A T T C C T T C A C A G G G A C T G T A C
EST39002 0	42	G A T G A C C	G G A C C C T T C G G T G A C C	C T G G C A G G G A G C C T G	C C T G C T A T G A T G C C T G G G C A G A T C C C G G A C C C T T C G G T G A C C J G A J A G G C T C C C T G C C A G G G C T T G G C C C C T G A C C G G G C T C C C A G C T C G G C C T G A C T G T G G A G G A G C T G A A A T A G C T G A C A T C C G C A A C C T C
EST39004 8	79	T G C C T A A G G A A T	G G T G G T A A G G C C T A A G G A A T	A T C T G G C T G G O G G C	C A C G T G G C C C T A A G T T C C G G G T C T C C T C A G T C T G S A T G G C T G T G T G G A A A A A G C T T G G T G G T A A G G C C T A A G G A A T T J A G G G G C A G G G G G C G A T G C C G C C A G A G A T G G T C C T G T A A G C C T G T G G G T C A A G A C C T A A C T T C T G G A
WI-16398	90	T C T C A	T C C C T A T A T T C C A T G A T A T T	G A A T G G T T G T G A A A A A T A T A T T G A T A T	A A G A T A A T G T C A T C A C A A C G C A A C A T A T A G A A C A T A A A A G A A A A A A A G A T A T C C A C C C T A A A A T C C C T A T A T T C C A T G A T T T T C A J T C J A G C A A C T A G T A T A T A T A T A T A T A T A T T T T C A C A A A C C A T T C A G T T A C A C
WI-16403	69	T C A C T	C C T T T G T C C T C A A T T T T T A A C	T A A G G C T A A T T C C C T A T A T A A A A A G	G G T T G C T T T C A T G A T T T T T C A T T T C C T A T C A G G T T T C T G G C C T T T G T C C T C A A T T T T A A C A C T T T C J C T T T T A T A T A G G A A T T A G C C C T T A A C T G T G G T A C A T G C T G C C A A A A T T T C C T C C C A G T T
WI-16406	24	C T A G G	G C T T T A A T G G C T A C A G A A A G A	C C A G A A C C A G A T G T G T T T A A A A A	G C T T T A A T G G C T A C A G A A A A G A G C J T G G T T T A T T T T T T T A A C A C A C A T C T G G T T C T G G C A G C A A G T A T A T T A T G C A T T A G A G C A A T A G G T G C C C T G A A

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCCTTTTATTCATGATTGTTTCATCTGAGAAATAACCTCCTGCTCTAATTTCCAA[C/G]ACTATGTT TAATGATGACTCAGTACTATATGAGACTGGAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGOC[G/T] TTCTCGGTACTATGTTTAAATTGCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCACAGCC AGCTCTGCTGCTGCAT
EST39366 2	72 T C		---	AGAAACATTTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCTAGA
EST39371 9	86 A G	CATTGGATT GGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGCTCAAAATCAATGCTTCTTCTAAAAGATT GACATTGCCAACCCCTGC
WI-17177	23 A G		---	ACAAAGTGACATATCCAAACCAACCIAGTCCATCCCCACCTGTGCCCTATTCTTCTTGTTCTTT AGAGCCCTTTTTCAGCTATTTCTGTGMAAGCAAACTGCACGAAGGCCCTCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTATTGATT	GGTCCCTTATG AAGCCACC	AGTTCTCTGGTTGCTCCCAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTTAGGTAATTTCTGTGGCTTTGGTCCACAGACACAATTAAGAAGATCAGGTCT GGCTGTGTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTCCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/J]CAATAACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACATTCA	TCCTGGAAAAAC TGACATAAAACC	AAAGCCCTGTAACTGAAGCTAGACAACGTCACACTTTTGGAAAGAAAATAACAGGAACCTATTATAT ACGTAATCACATTTTACATCCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGCC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACCTGAACAGAA TGCAGGAGGGTG[C/J]AGAGGGGCCGAGATTGGGTGTTTTCAGGGCAGAGAGTGGAAGACCCAG
EST39501 0	81 A G	AAAGATTCCCT GTAGACATCT	CAC TTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACACATTTTGACCAAGCCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAA TTGCAAGTGCAAGTTCAAGTCAAAACCAATTCTC
WI-18387b	84 A C		---	CACAAAATGGGACTGCTGAAGAGTGAGAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CAIGCTTTAGCCATAC[C/J]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATAC(A/G)TTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTGTGAAAGTGTAAATGTGGCGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGAACCT GAAACAC	TTCTTGAAGA AAGGCGTC	TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGTGACTCGCGTGGA ACCTGAACAC(A/G)GACGCCCTTCTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCCCTC ACACTGTTA	TCCATTGAGTGATCACATCTTCAGGATAGGT(A/G)ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG TCA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA(C/T)GTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTTCACAAATTTCTCATCAGTGTAAATTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATCTCAGC ATTGCTATAAG C	AGAGAGACAAACAGAAAGATAAGGGAAATGGGAAACAGAGTGAATTAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTAAGTCTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTC TTTAAATTCAC TC	AGAGAGACAAACAGAAAGATAAGGGAAATGGGAAAG(C/T)AGAGTGAATTAAGCAAATCTT GGATTGAGATTCCATTAAACAGGAAGTTTCTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTAAGTCTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATTTC A	---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCTGTG CTAGACAGATTCA(A/C)TGACACACAACACAGGAGTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	AGACAGATTTC A	---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCTGTG CTAGACAGATTCA(A/C)TGACACACAACACAGGAGTGGGGTACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT C	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACATAAAAAGGAAAGGAAAGAGAAATCAAGGGAGGCCAAAGTG GGAAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCCTCTTTGGCTCTAAGTGGGACTA(C/T)TC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGTGGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCCTGATGCTGTGTTGTGCACATTGGGGCCACAGT(C)AAATAGGCTAAA AGGCAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA G	TTTAGGCTTTG AGATGGTTTCT	GGTGTATAGCTGCTGTACACCACAATGGCAGAGGTGA(A/G)TAGAAACCATCTCAAGCCATAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCATCTCGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGAGGGTGGGGCCCGGGCTGAGGGTGGGGTGGCGAGG(C/T)GGT CACTCCCATCGTGGCCCTGGCCGCTCCCTCCACTCACCCACACTGGCCAGTCCACAGTTGAGGT

WI-18491	109	A A C A A T G G T A G G T G G T A T T	C G T G T G C A T T T T C T T G T A T C C	C T A A T G A G A T A A C A T G A A G G C G T T A G C A C A G T G C C T A A A C A C A G A T A A G T A A C C A A C A A T G G T A G G T G G T A T A A T A C T A T T A T T A A T C C C A G A T G A C [G/A] G G A T T A C A A G A A A T G C A C A
EST50757 b	79	C A G C T D G A G G T C T G C T T C T	A C C T T C A C C C G C C C	O G T A G C C C C T C C A C T C T G C T T C C A C A A A G T G G C T C C C G A G A G C T C G A G G C T G C T T C T T T T A T A T G T G A G G C C C [C/T] G G C G G G T G A A G G T C A G A G A
WI-17675	103	G G A C A T T T G G T C A T G G T G A C T T	G G G G A C C A C C C A G G	G A T C T T G A A A G C A C T A G A A A C T A A A C A T C T T C A C C A G G T G C T G A A G A A A G T G C T T C G T T T T A A T T G C C A A G C A G G G A T G T G G A C A T T T G G A T G G T G A C T T [C] C C T G G T G G T T C C C C A T A G A T T C A C C A T T G C C T C T A A T G G T G T C T A
WI-16543	67	A G A T A A A C T A C A T T T G G G T T	G A T T C A T C A T T A C A G G G A C T T	G A T C C A T T A C C T A G G T A A A A T T C T C T G A A T G T C A A A C A A A G A G A T A A A C T A C A T T T G G G T T T T G G G [A] A G T C C C C T G A T G A T G A A T C A A G A A T C C T C A A G T C T G T T G C C A C C C A T T T A A T A C G T A T T T T T G T T A A G G C T G A A G T T
WI-17687	107	G C C A A A A A G G T T G G G G A A	T T A C T T T T G T A C C G A C C A G C A	A T C T G A G A T G G A A G A G T T T C A T C C C A A A C C A T C T C C C C T G A C C C C A G T C C A T G G A A A A A T T G T C T T C C A C A A A A C C G G T C C C T G G T G C C A A A A A G G T T G G G A A [C/G] T G C T G G T C G G T A C A A A A G T A A T T
WI-17690b	79	A G C ... A G G C A T T T T T C	...	A C A A C A T G T G A A G A A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T T C T A G C T G T T T G A T T G G C T C C C T A T A G [G/A] T T C A G G A C C C A T A A C T C T T G T T C A C T A C T C T G T A T G C T G T G C T G
WI-17690a	63	A G G C A T T T T T C T A G C T G T G T T T	C A A G A G T T A T G G G T C C T G A A T C	A C A A C A T G T G A A G A A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T T C T A G C T G T T T G A T T T T T G G C T T C C C T A T A G A T T C A G G A C C C A T A A C T T G T T C A C T A C T C T G T A T G C T G T G C T G
EST51717 b	128	G C G G A A G A C A T T G A G C T G T T	T T G A G G C A A T A A T C C A G C T C	G A T C C A A T C T C A G T G T C T A A C T A C T C C C A G A T T A T T C T G A A G T G G A A A C C A C C C T C C G A C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T T C T G G G A G A G G C A G G C G G A A G A C A G T G A G C T G T T C [T] G A G C T G G A T T A T T G C C T C A A A
EST51717 a	39	G A T C C A A T C T C A G T G T C T A A C T A C T A C C C A G A T T A T T [C/T] T G A A G T G G A A A C C A C C C T C C G A C C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T C T G G G A G A G G C A G G C G G A A G A C A G T G A G C T G T T C G A G C T G G A T T A T T G C C T C A A A
EST53012	97	T G G T C A C T T T G T G C C C	G G C T C T G C C C A C G C C	T T T C A G G T T G A C A G G T T T A T T C C A C C C C T T C C A T C C C C A T G C C A C C C A G G C A G G A G G A C A G G T G C T G G A G T G G T C A C T T T G G G G C C [C/T] G G G T G G G C A G A G C C C A C T G G G T T A C A T T C T C T G T G G G C A G G T G T G G A C A C
EST53349	96	T G T T G A A A G C A G T C A C A A T G A G T A C	C A T C T G G A T A T C T T G T C A C A T T T T	A A A C T G C A A A T A C A A A C A A A C A G A A G T C C A A G A A G G T A A A G T A A G C T A A A G T A A T T A C A C A T G A A G T A T A T G T T G A A A G C A G T C A C A A T G T A C [A/G] A A A T G T G A C A A G A T A T C C A G A T G T T T A A T T T C G A A A T G T C C C A T G A C T T G A C A G A C T G A G A G C C A G C C A G C C A G C C A G A G A C C T G C A G A A C T T A A C A C [A/G] G A G C A T T A T T G T A G A A A G G G C A A G T C T T A C A C T C A A A T A G G T T T T A A C A T G A A C A C A T T A A G G G A G A T G G C C
EST53389	74	A G C A	C	

[illegible]

TGR- A003P30	117 C G ---	---	ACAAGTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCATTTAGAAAAATGCAGTTTAAAGCAGTGTCA/C/G/ACTGGCTGCCTGMA GGTACCCCTGGAGATACT
TGR- A004S34	156 C T A	TTAAA	GCTTGCTTTTATGTTAGTTCGGGGGAAAGGAGGGGCTGACAAACCGCAGACATCTGGACACACAGC AAGGTCAGGGGAGTTTGCAGAACTCTTTGCTCTGGCTAACAGTCTGTCATGTGACAAATAGCCA AACCTCTCTCATTCCTATATAA/C/TCTTTACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97 A C ---	---	AACACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT/C/JAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAGAACAATATAG
TGR- A004T44a	69 G A TGA	GGAAGATAAA CCAAAATGAT	AACACAGTGTAAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAATGAT TGA/G/ATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAGAACAATATAG
TGR- A004V08	60 T C	CAGGAAACA GGCATTCTCT	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCAATCTCTTA/T/C/GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAATTTCAA
TGR- A004V28	125 A G ---	---	TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATATGATTATCTTCACATGA/G/JAAGGT TTCAGTTATAAATGCTTAAATCTATCTATTGCTTAAATCTGATCTATTGG
TGR- A004V28 a	29 A G	CGATCTC	CCAGGCTATAATGTTGGGGTGGCATCT/C/J/GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTG TATTTTGTAGTAGACATTTGATTTTGTAGTAGACACAGG
TGR- A004X20	25 T C GA	GAGAC	TAAGTTTCCTTCTCTCTGTAGGA/T/C/GCTCCATGTTACAGTCAACTATAAACACATGGGCTCATGT TCACCTGGGCTTCGCTTCAGAGGAGTTGATAATTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTCAATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TGR- A004X30	26 T C CCAC	CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC/T/C/JACTAGTAATACITGTAAATAAAATAGTTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102 T G ATGCAAACT	AAGCAA	CACGGTATAGCCTTATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCACAGTACCTTCATTTGGGTATGCAAAACT/T/GTTGCTTTCATGAAATTTCTAATTAAAGG ACTGTGCTTCTTCATATTCATATGAGACATATACAAAATAACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGTATTAAGACTG

-221-

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTCCCGATGACCATCTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTAAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGCTGCCG GTCC	GTCITAGCAGAGGAGATAACTTTGAGGACAGCCCCAACGGGCCAGGTAGCCTTCAGGGGGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTC
TIGR- A005D17 c	81 T C		---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAAATAGACTGAGAGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTGGCTCTCTGTGAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGCCAA GAAGATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAAATAGACTGAGAGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTGGCTCTCTGTGAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTAT GAACCTTAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAAATTTGGTCATCACTGAACITTTGCCCAATATATTTCTATACAACTT AACATTATTGAACCTTAAACTGTACACTGTGTGGCTTTAAATAGACAATGATTTTGG TCTATTACTTAGTATAGACAAAGTACTTTGTAGACAAAGTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTCAAAATTTATAACAGGCTCTGTGACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCACCTGCCCTGCCATGTGGATAGTACTCTTTGCCCTGCTTCCCTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC AGAG	---	CTCAGTGTAAAACTTTGTTAGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTGGCTCTTTATTTGTTCTTTCAACAGGACC CCACAGATAATTGCGGTATGTCATGAGGACTGGGATGCTCTCTATGTGCTGGATGCTCTATTTT
TIGR- A005E42a	42 A G		CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAGTCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATGTCATAGGTAGTAAATATGTTGTTAAGAGAATCCACAAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAAATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGACCTGACTCGG TGCTTTACAGTACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAACTGTCTTAGGGTGTCTCCCCACAGAGCAGATCTTGAACCG ACTCAATTCCTGTGTAAAGAGCAGCTTTGCTCTGCTTACGGACCTCCCAAGGTGCGCAGATCTAT ATAGGATGCTGGATTAGTCTTTGATATTGTAAAAATTTCCCAAGAGCCGCATATGTAATCTGCC

-222-

X57830	106	GCCT	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTACCTATCTGTGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGAACCAACGATCATATCTGCTATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTAGCTGTGAG CTTTC
X74070b	72	TGTGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCTG/GATAAAATCTAGATCTCTAATATTTTAAAGCCAAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATTTCTTGCAGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44	CT---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAAGCTTCTCCGGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAGG TCCA
D28513b	133	AG---	---	---	ATGACCAAAGCCACCACATTTAGAACCTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTGTGATTGACTGCATGAATGCIW GJTGCGGTGAAGCATGAACCTTTGTTAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	AG---	---	---	CCACTCCATCTCTGATGCCCAAGTATCCACAGCCTCCTCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAAAGTCTCCAACTGATCCTACCTCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	AG---	---	---	CCACTCCATCTCTGATGCCCAAGTATCCACAGCCTCCTCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	GA---	---	---	CTCCTGCCCTCCTCCTCCTGCCCTGTGATGCTCCGCTCAAAACAGCGGAAACCTGTCTTGAATGGGG GAGGGGGCGTTTG/GA/CITTCCTTCTTGGCTTCTTATTCCTCACAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCTCCCTCAGGCCACCTCCTGTCTCCTCCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	TCTC---	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTCTGCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATACTCATTTCTATAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAAGCTTCC TTT

D63807	101	C T	---	---	CAGCAGGACTTCAGTGCAGTATCCCTCCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTCTGTTCCA/C/TGAAGAGGACTTTTGTTCACAAATGGATCAC AATGCAAGGAGTCTGTTCTCCCTCCCTCGGCTCTCGGCTGGGAGGGTGACCTGTCACAGATGAC
D90145	21	T C	---	---	TGGAAACATGGGTGAGACCTC/CJACAGCTACCTCTCTATGGACTGGTATTGGCCAAACAGCCACA CTGTGGGACTCTTCTTAACITAAATTTAATTTATATACATTTAGTTTATATAATTTATTTTGTAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTCCCTCGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T C	---	---	ATTACACTCTCAAAATTTTGGTGTGIGITTAAGTACTTCTTATTTATGAGCCCCC/T/CJGAGGA CCAGACATGTTATTCAAGCCCTTATATACCATCTAAT
EST16668 5	71	C T	---	---	GCATTTTAAATTCACATGGAATCATTATTTACTATTTATGATGTTTACATAACAAATTCAGTATCAT ATG/C/TJGTAGATTTTCAGATGTAGGTCTGTCATCTAGTCACTTATCT
EST16904 7	57	C T	---	---	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAATTAACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAACAAT
EST21863 9	49	A G	---	---	TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAACTGATACACCC/CJG/TTACTACTTACTC TTCACTCTTCAAACTGATCCCTAAAGACTTCTACTTAGCANA
EST21885 6	80	GA	---	---	GGCTGAAGTAGAATCAAGGTAAAGAACATTTTATGCACTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGG/CJ/TGTGACAGTGTGACAAAACACAA
EST22623 8a	26	A G	---	---	ATTTAGTGCAATGACAAAGCCCA/CJGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCATAGATATACGAAGTTAACACAAAGTATGGGAGT
EST22644 2	98	A G	---	---	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/CJAAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31	T A	---	---	CCCTCATTTTAAAGAGCGGACATAAAAA/TATATACAACAAAAACCCAAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	T C	---	---	AAAGATCTGGCATTATTCACATCATCTAAATATTTGTAATTTACTTTTCCATGAGTATTTTTC TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT/CJGAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAAT
EST24308 3	45	A G	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/CJG/CATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAAATATAAACCTCGTTC
EST24435 6	73	GA	---	---	CTTGAACCTCTGGTCGAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/CJG/TGCCTGACCCACATTTCTTTATCCGATCTGTGTGAGGACATTCAGGTTGTTTC
EST25089 6	25	T C	---	---	TATTGTGCATTATCAAAATGGTTA/CJGAGTTTTCATTAATAAACTGTAATGATTCTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACATT

[illegible]

EST33508 1a	36 A G ---			AAAACATGCTATTGAAACAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTATTCTTGTTTTGAAAAATTAATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAAC[C/T]CTTTGAACACTACAGCCTGAATCCCCC
EST34739 3	97 T A ---			GAAATATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTCTAGGCTGGGGAACTCT[A/G]GGTGCCCTTACAACCTCCAACTACTGCAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTG[A/T]GCTTTCTGGTGCCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCACCTTACTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[C/G]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCCTTTCAAAATTTTGATGAGGCATTTAATG[C/T]ATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTGGCACCTTTCCTGTTGTG ATGTGCAAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGTTCCATTATATAAACTGAGGGAACAACGGTGTGACATGGCAGACATTTATTCATGGAGA AGTTCTCCCATGAACCAAGA[C/A]CTTGCTCTCATGATAAGTGGAGACATAAAGAAAGCCAGGT ATATAATTAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTAGCCTACAGC AGTCAGAGGCGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCCAACTGATCTTCA GAAAGAGGTACACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTCTAGTCGT

EST36620 6	50 G A ---	---	GAC TTATTAGATAAGGGGTTTCGGCTACCCCTCAAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATATGGAAATAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCCTA[C/G]AGGGGACATATCACACATATCTTAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCATTICA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGCCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATTA[A/T]CTTTTATGTTCTTCTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAATTTGAGGGGACATGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTCACTCTCTTGGCCAGGACGGTTTGAACTCTCTGAGCTCAAGTGACCTCCCACTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACACTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGTACGGGCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAATTGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTGAAAGTCT[T/G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGA GCTCTCTGGATAATGTCACCTCTAGGA[A/G]TAGTAAACAGGTTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCCTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGGTCTTGTAGCTTGCTCGGCTGAACATAAGATATCTCTGCTCAGCCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTTCAAGGCACTCTAGTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAATCACAGTGTCTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACCTCTGGGTTCAATCACAGTGTCTGTCTCTGCAAGGCTGTCCTCAGGCAAGTTGCTGACTTCTCTG GTCCAGG

-227-

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCGTGAAAACT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAAATCAGTTATGAAATATAAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCGCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCAATTTATTTAC/AJGJGTCATGAATTCATTAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACITTA/TGJTATCTCA ACAATCTTGAAGGTGGTATTATTTCCCGGCTTATAGGIGMAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGATATCTGTATATGCTTTAAGTGGCATTTCATGTCACITTA/CJTCGCATGG AAGAACGCTCTCCTTTTAATCCCTAACTCTCTCTCTGGAAGACAGAACGTCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCTCTTTTCAATTAACCAAAACAAAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACTGACTGAC/TGCTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCGGGT/CJTGTCCTCGGATTAGGCTGAGGAAGACATTACTTCCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGACAGCCA
EST39053 6	90 T C ---			TTTTTTGTTACTCTGTAGCCAGTCATTATCTGAAGGTTTAAATATATCATTTTATGGGATGAGATCA TAGCTTTACACAAATGCTATG/TJAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCCTCTGCTCTCTAGCACTCAGACCACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG/GC/GJGTTTTAGGGAGAGCTGGCACCTGCGCTCTAATCTTCCTCTGCCATTGACCAGATGGGT GCCCTTGGATACACT
EST40544 7	31 C A ---			GTCACCATTTGACCTTACATAGTGCCTCTAGT/CJACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/TCTCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAAGGCTCAAGGTGTTCC AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTAGGCATGCACA/VJATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTACATTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACATTTTGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTATCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA/VJGGACTTGGAGACAGCGATTTAAATACGGAACAAAGGCTTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/VGJCTGTACTCCCAATATCCTATGTTTTAAGCT

-228-

EST51340	51 G A ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGGAGGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGMCCTCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACACTACT/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTCTATCCATTACCTCAAAGCAGTCAATCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCCTTC ATTGAGCCCTTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCAOAGTTGCAGCAGGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C/T/CJATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTCTATGGATGACTTTGAGATTATCTTTGTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTGTCTGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAGAAGAAAGGCTTTGGCCTGGTGGTGCCATAGGCCTGTATATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCTGGAAGGGAOCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCAGCGTCCCCAC CC[G/C]CGTGGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGMAGCAGCTGCCACCTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAATAACAGTAGTCTTTTGTATTTTGTATATT/GJGCGCTGA AGATCATCCGCAAGGCAAGGCTGGAGGTGCGGTGGCCCTGTGTCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGCTCTCTGCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAACCTGGTTGCCAGCTCCAAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTCCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAATGTCT AAGGT

M148728b	111 T C	---	---	AAGTGAACAGAAAGCAAAGATGGATTGTTCTATATAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAATCAGAAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGCTCATCTGTACCTTGGAGATCCCA GTC
M18079	52 GA	---	---	GCGCAGTCCAAAATACAAATTGGACAGAGAATCTATATTGTACAGAACTGAGTATTTATTCACC CCATCAAGTATAAGGTACTGATTGATTGGTCTTTTATTAACATTGGTATATTTCCATTCAATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C	---	---	TAGGGATCTGCGCAGGCCATTGCGACAGCCACACACCCACTCCACCCCTGATGCTGCCACCC TGGACTGTGGCCCCCAACCTCGGGAGGCTCCCATGTGCCGTGTCGCCAAGAGACAGACAGAG AAGGCTCAGGAGTCCTTTGTGCTCAGCAGGGCGCTCCGCCCTCCCTCTTCTGCGCTTCTAATA GC
M21539	114 T G	---	---	TCACCTCGTCCACAGCTCCACCTGCATCTTCATCAAAAGCCATCCAGGGATACACAGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCATGATGATCCCCGACAGCAAAATG/GTGTTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G	---	---	CCTAGCATTTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATATTTCCCTGACTTC CTGATTTTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G	---	---	CCTAGCATTTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATATTTCCCTGACTTC CTGATTTTTTCTTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G	---	---	CCTAGCATTTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCCTCACC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATATTTCCCTGAC TTCTGATTTTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTAACC TAATTCCTCAGTAA
M63967	57 G C	---	---	TAAGGCAGCTGTCAGGGAGGCCAGTACAGTCCAGCAATTCACAACCCCTTGAC/GCJAATGCT TGCCAAGCTGTTTTAAAGCCAAGAACACCCCTTTCTTTGTGCCAAATTAACCTTAGAAGAAACCCCA CAAAATAAGCAATTCATC
M81695	34 GA	---	---	ACTTACTTACCCTCACCCTGACGGTACGGGTGACGGGGA/GAAGCAACTGCACACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTTGGGAGAAACGCTTGTCTGGGAAGGGCCCTTGTCTGTCAAGGTTCT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTCCCAAAAGGACTTGACTTGCATTTCTACCT

U06641d	166 C T ---	---	CTCCCTCTTTATTTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTCCCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAATTTAAAAAGATCTTTCAAACTTACCTTGTAAAGACAAAATTT TATTTCCAGGCTATTAATACGTACTTTAG[C/T]TGGAAATATTCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCTTATGAGGTCCTCTACTTCAGGAACACCCCA[C/T]GACATTGCATTTGGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCCTTGCATTTGTTAAGTTCAAGACAGATGGGCATATGTGTACAG TGGGGCTCTCTGAGTCCTGGCCCAAGGAAGCAAGGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAAGGCAAGAGCGGCAAGATGATTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTC[C/T]ACATCTGCCCGGCCCTTCCAGCCCTTCCCCAGCCCTCCTCTTGTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATCTT[C/G]GCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGGTCTCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAATGAACCTTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAAATCCAGTTTCAATTTGCTATCTTTGTACCTTGCACAACTGTTTAAAC CTCTTTGTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGAGGATAGTGAAGTTACATGT AAGCACAGAGGAACAGCCMAGAGAT[C/T]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTTACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACAGCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]TGGTCTCATAG CTCATATGCAGGATTCATTCA
U17077	122 T C ---	---	TCCAATTATGGTCCCAAAAGCAGCTTCCACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAC[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAAAACAACCTGCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCCAGCTGGGTAGTCTAGAACTTT[C/T]AGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164 C A ---	---	---	TCAC TGT GGCCTCATACTCTTTTCCATTTTCTACAAGACCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGATATGACTTTTATATGAACCCCTTCTTAGG GTCCAGAGGAATTGTGGACTGA
U25975a	143 C G ---	---	---	TCAC TGT GGCCTCATACTCTTTTCCATTTTCTACAAGACCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAAC/C/GAAGAGAAAAATTGCAAAAAGACAAATATGACTTTTATATGAACCCCTTCTTAGG GTCCAGAGGAATTGTGGACTGA
U25997	61 A G ---	---	---	CAGGAGAGGTTATTCACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCTGGTTTGATTTTTTAAAGTAGTTCTTATTTCTATCCCTTTAAAGAAAAATT GCATGAACCTAGGCTTCTGTATCAATATCCCAACATCTGCAATGGCAGCATTTCCCAACCAACAAAA TOC
U28413	29 C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCTCTCATGTTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTCTTGTATCC CAGATGTTGTGGCTGGAAAGCCCTCATTTGCTACAGTACAAAGTAACAAGTCGTTGTACCTCAGTT G TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTATGATTTTGGACCTGCCGTATATCTGTT CTTCTATCCACGTAGCCAA[G/G]TTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCAACAGTTGAACACAAGT GCTGTCA
U30884c	89 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC[G/G]GTGATGATTTTGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCAACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCCGTCTCAA[G/G]CCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCC[G/G]TCTATAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCC[G/G]TCTATAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCACAGCCGATTGCGTTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCA[G]JCCACAAATCTGGTGCCTCTCTCTGCTTACAATGTCTAGGTCCCACACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCC AACTAACTGGCTTACTTCCT
U31416b	68 CT ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCCTCAGCCCAAAATCTGGTGCCTCTCTCTGCTTACAATGTCTAGGTCCCACACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---	---	---	ACGGGTACACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCTCC AGACCGCAGG[C]TJCCCCCAGCCTCAGGTTGCTGGAGCTGCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTGTCTTCTATCTGGGGGACGCTGCTCGAGAGAGCGCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 AG ---	---	---	GACCACGCTGAAACCCACCCACCCGCTGTGCTGAOCCATGGGCCCTGAGGTCCTA[G]JCCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCCTGGCCGACGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCCTT
V00540	39 TC ---	---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAAGGCACCTAGTCCCTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	---	TCAAGAGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACCTCTGAGCCTCTCTGAGACCATGTGGTTTTTAAAA/TATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAAATTTGGATTCACTCTCTGTTTTTTCATGTCTCTCTT GTAAACCCCTGAGATCATCAG
X52011b	148 CT ---	---	---	AGGAAGATCCCACCGACCCCTTCTGGCCCTAATCCTTTAGATTAGGTACATTACATTATAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTCACAAAGAAAGTTGGGAAATTTGGG AAATCTGTTGTGCA[C]TJGCTC/MATGAAACGCCCTTTCGGCTTTGGGCTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 AC ---	---	---	AGGAAGATCCCACCGACCCCTTCTGGCCCTAATCCTTTAGATTAGGTACATTACATTATAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTCACAAAGAA[A/C]GTTTGGGAAATTT GCGAAATCTGTTGTGCAAGCTCAATGAAACGCCCTTTCGGCTTTGGGCTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---				CAGGCCACCTGTCTTCTCTCCACAGTGACACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCAAGGCTCCAGGCTCCAGGCTGGGGCTTGGCAGGCTTGTCAAAATAGCAAGGCCAG GGCACAGCTGGAGAGCATCTTGTCTGGCAGGGCTTGGCCTTGTCCACAGCCCACTGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---				AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTTATTTTCTCTTATGATACAAAATCTAAATCAATATTGAAATAG GATGACACAATTTACTAAATACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA GCCGTCTCTGACACCTCCAGAACGAGGTGCTGGGCCCCGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGAAGCCGCGAGGATGGGCCCCAACTTCGCCCTGCCACTTGACITTCACCAATCCCT TCCTGGAGACTTGAAACCTGGTCTCAGGAGCGAAGGACTTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGATGTGACAAAGCCTTTAAGCGGTTGTACACTTGATTGTATATAAGATAATTTGTT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAAATTTCTCATAGCTTA TTGCACAGGAAAGCATTTTATCTTGAAGAAATTTGTATAAAGAAATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---				CTCAACCCATAACTCAACACATCTTCTTCTCCACCCACATCCACACATCCACCTCCATCC CCAAACCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAAACCCAGGCCATGCCCAACCCATCCCCAAGCC AAACTCAACCATCC
X78932	62 T G ---				ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCCCTGCTTGGCCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTCTAGCTACTTCTCTGCTGCTGCTTGAAGACCCCTCCCACTCTCGGCTCA CATTTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG ACCCAACTCAAGTCCAGGCCCCAGGCATGTTCTTCTGCCCCCTGCTTGGCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCTCGGCTCA CATTTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG GGCACCCAGAGTACCACAAAGTCCAGGAGGGGCGGCCCTGCGCGTGTCCGTGTTTCTTTT CAGCCCGGAGAGGTCTGACTGGGGCTTCTCCAGGCTCACTGGCCACCGTCCCGGCGGCTCT CTTTCTCCCAAGC[G/A]AAACCAATGCGCCCCCTTCACTCGCGTGGCGGTGGAGGGCGGGGGCTT CTTTCAGAGC
X80026	25 T C ---				ACCACGACCATGGTCTAGGACATGGATCGGGTCCCCCAGACGTGTGCACAGGGGACCCCTCTGCCC CACCTGGGCTTTTCAGATACTCTGACCAAAAGCCTGCTTTAAACCGCAAGATGGGCGCTTGTGGGC ATGCGCAGGAGGAGCCATCGGGTACTAGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X80197b	99 G C ---				
X80197a	28 A G ---				
X85106	150 G A ---				
X87160	128 T G ---				

[illegible]

1282	130	CT	---	GTGGATACCACTACAGTCTAATTTTCAGATGTTTTCATTACCCCTAAAAGAAATCTTGACCCATTAGCAATATCCCTGCTCCTCAGCTCAGCTCCTTATCGCTATAGATTTGCC[CT]ACTTGACATATCATACAGATGGAGCCATACATATGTGTGCCCTTCATGATTTGGCTTCTTCACTGAGAATAATGTTTTCAAGGT
6810	68	CT	---	AGTATCACACATCTTAATATATTAGATATACACATAATAAATCACTCCCTACCTTGAAACATTTA/C[CT]AGAAGCATTTTAAATTTACAACACAAGCTCAAAAGAACCTACAAATAGTCTAGTAGCTGTTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAATGCTATGAACAAGTACAAATTTCTTTTGGAGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118	AC	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGTAAC[AC]TGTGGATACCCCTGTGTGCTCTACTGGCCTCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTCAAATCTTGGTTCAGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212	C	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166	GT	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[GT]CATATACAAAATTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39	AG	---	CTGGTATGTCATAAGCAATCCATAATTTGTTATAGCTATT[AG]TTACTATGGCACCAATTTGGGACACAGATTATATATGTCAGACACCAACGAATGCTCTTAAAGATATGCAGCAAGCACAAATCTGTCATGGTTAAACAAAAGAAATGAACGCTAGG
6972b	149	GT	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATGATTATGGCACAAATTCAGA[GT]CCTGTTATTGGTCTATTCAGAGATCAACTTCTTCTGGTTAGTCTTGGGAAGTGTATGTGTCGAGGAAT
6972a	122	AG	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[AG]CTATTGATTATGGCCACAAATTCAGAGCCTGTTATTGGTCTATTCAGAGATCAACTTCTTCTGGTTAGTCTTGGGAAGTGTATGTGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTAATCTTGAGGATGCCCTTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTCCCGTATTTCCCT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCCAAGCCA/GJAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACA/CJCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTA/GJTGATTTACAAAAGACACCCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCTATCTTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTGCTGCTCCTAAGGTCCTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTGCTGCTCCTAAGGTCCTCAAGGTCCTCCCAATAA/TJCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAAACTGTTTAAAGTAGAAAAAACCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCC/GJCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAAATGGCTAGTTACTTGCAATTTTGGCATTTGTTAATCACTGAATC TGGGTTTCTCTGAAATCCACACAGAGCATGCACCTACACAACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTCTCTAAACATCAGTCCACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTA/CJTGCTCATCCGAACCTCCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTAATCTG
8467a	70 A G ---	---	AAGGCTTCTCTAAACATCAGTCCACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCATT TG/GJCGCAAAATCCACTTTGCTGTAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTAATCTG
8498	84 C T ---	---	AGGGTTCAAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/CJTAATACTTCATTAAATCGAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGCTTTAAATAAAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAAGTCAAG

WI-18562	29 GA ---	---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTTCTTACATT TAGCATTATCAGAAACGA
WI-18618	51 AC ---	---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTAAATTTGTAACACACAGTGCTCGCACAGTTC AC
WI-18683	22 CT ---	---	---	TAAAGTGTTCAGGACTGGACTC[G/T]GGTCCCTTTATTAGAGACTGACAGGCCAGTGGGTCCACCCAAV CAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75 GA ---	---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATAGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTAACCCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94 AG ---	---	---	AAATAAGTTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTCACTAATGTGAC[G/A]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 TA ---	---	---	GTCTATTCAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC T[A/G]TGCCATAATTTAATCAGTGCCATATTGAAGACATTTGGATCGTTCCAG
WI-18723f	94 GA ---	---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ---	---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ---	---	---	TTTATTACAATATTAGGTGGCACATAACTAAACAGCTTCTGA[G/A]ACAGGAGGTAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18619	44 GA ---	---	---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAGGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA
WI-18715	76 GA ---	---	---	TGGAGCTACAACCAACCCCC
WI-18535	107 GA ---	---	---	GTAATAAAGTTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATGACATCTGCTGTGGCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGTA[G/A]TTGTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107 CT ---	---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTGGAACTTCAGTTTCTTCATAGATGGAAG[C/T]GCTATACCTTACCTCGTAAAA GTCTGATGAGGAAAGATTAACTAATAGATGATGATGACCTTAACAGAGTGATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTCTACCAGGCAGACGAAG

DWU-133c	313 A G	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T	TAATTGGCCACTGCCCTTATTATACAAAACAGAAATGCTCATGACTTTTATGTGTTACCATCCT TTAATAGATCTATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGGGCGAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T	ATGAGATCCTTTAAATCCTTCATGAACGTTTGTGGTGGCCACCTCTACGTCACAAATCAAGTG TGTTTCTTCAGTGATCTGGGAAGATTTCTACCTCTGACCAACAGATTCCTTCAGCTTCCATTTGGCC CCTCATTTATCCCTCAACCCAGCCACAGGTGTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAGGATTCATGTGGAATATAAAGAT
DWU-387	169 G T	GTGTATAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCCTGCCAACAAAGTTCACCTCATATATAAAGCATTTATTTTA CTCTTTGAGGTGAATATAATTTATATTACAAATG(GT)AAAAGCTTCTTAAATACTAAGTATTTTCA GGTCTTACCAGATATCAAGTAATAACACAAATGAAGTGTCTATTATCAA
DWU-447b	172	ATTTTAGTGTCTTTGGTTAAAAATCATTTGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CCATTATTTTTCATTTGTTGTTCTAAGAGAGATTGANAATCAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-447	85 A G	ATTTTAGTGTCTTTGGTTAAAAATCATTTGCAAAAGTATTCTGAACGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATGAATCACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT CAACCATATTTTTCATTTGTTGTTCTAAGAGAGATTGANAATCAGTTTAAATGCTTTCTGTTAG TTAGGCCCTTCTTCTTACATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-476	63 C G	GTAAATTCAGTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATTAAGGTTTAAAGTGAGTC/GAT AAATCAACTGTCATCAGGTGAGGTGCTGCTCCATACCCAGCGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATCTATACCATACAAAATTTA ATTTGACAGTATTTATGTTTAAAGCACAGGTGTACCGAAAAGTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGTACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCAATTCGAATCTGTTTTCAATGATTTATAGAGGTTTACAAAAGTGCCACTTATTAA AGAGCTCCACAGTGAAGATGGAAGGTGAACCTGCTTTGAATATCCAGATGTTTTGGTCT[AG] TGCGTATGGCAGTGAGCAGGTATGTTTTGCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTTATTCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATCTAGTCCTGATTTC
DWU-59	94 C T ---	---	---	CATTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAAGTCACTTGGC/CJGAGCCGTGTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGCTTCTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAAATTTTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCCTCGCCTGCATTGCAGAAGGAGAGCAGGTCCCTCCTGGAGAA/CJTG CTGGTTCCCCAGCCCCACCCGGCTTTCACACACACAGGCTGTTGAGCAGGAGGTGGGTAAAGAGT AGCTGTAGACCCCAAGCAACCAACCCAGCCCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTTGTGAATAGCTACAGAA/CJGAAATGAAAGTGCACCATCAGAGT GTAATTAGGCTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAATTTTAACTTCTTTCATAA/CJGCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAGTT/CJAAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAATTTTAACTTCTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAGCTTCCCTAACTGTCAAACCTTTCATTTACTGAGATTTTTCAGGCCAAT GTGTC/JTJGTTGGTCTGAGATTTGATTATCAGCTGGGTAAAGTTAACCTGTTCCCTGTTTCA

WI-18063	105	GA	---			AGGCTTTAACTGATAMCAATTTGCCCTTTAATCACAATACAAAACTCTGCACATTCATCCCTCCTTC CCATGTTTTCTGATTTGATGTAAACTTTAAATTTGT[G/A]TCTTTTAACAATATACTGTAGCTGCA AGTGAAGAGATCAGAGAGGTTATGGTTGGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT TTGTTTTTTCAGCATCAG[A/T]GTCCTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT CCAAGCTCACTCAAGTATTTAATCATCTGCTAATTCATCCCTTTGTTAATTCATCCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTGACTT[C/G]GGGCCCTTTTATACCTCCCATATCTCAACTTGTAAAGC GCAATCTGAACAGTTTTGGTAGTGTATTACAGAGGAT[C/T]GTGAAATGAGTTGAAATGAGTTGGAGTACTTAC CACTATTCATCTCTGAAATAGTTCACTAACCAAACTACTGACAAACAGTTTAATTTTGGTCTCT TTCAAGATTAATCAATTGGAAGGGGACCATAATTCACCTTTTAAATCGAAAAATATCTATATACT T/G[C]CCAAATAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA GCATAGCGTTGAGGGGTGTACAGAGGAGAACCCAGATTCACTGCTGCTGAGGTTAGTCTGCGGGG GT[C/G]CGCGGGATGACACACACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG TCAATCTGAAAACTTCTGTAAGCCAGCATGGGGT[G/T]GGGAGGTGATTGCTGGGGAAGATG GGCACTCACCGACAGCAGCATCTAGCACCACAGTACAGGGACGTTGAGGTGGCAGAGGGCTTT ACAGATGTCAGTTGTTGAAATGGCCATTAAAGTATGGGCTTTCTTGTAAAGTCATTCCTCAAA AGGCTTGGCAAGAGTTTGCTATACAAAGGAGGACAGAGAAACATG[A/G]CTGGGAGTAGGCTCT GACAGAAGGTGGCTGTC
WI-18078	86	AT	---			GATTGAAGGGATTGCTTTATTAA[G/A]TGAAAGCGTGATAGAGGAACGTGTTAAGATAAAACA CTTATAATACTCCCAATTGTAGAGTGAAGATTG TAGGAGGGAAGGAGGTGGCTGCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTCCCAAGC TTCTTACTTCCCAATAGAT[C/T]CTGACAAATGTCTGCAGAAAGCTCCCAACCTGGAAC TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT ATCTATTTGGGTCTGAGAAATCCACAATTTTGA[A/G]GAATTTCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18091	90	TC	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT ATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18119	38	TC	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT ATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18142	66	TG	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18178	68	TC	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18244	35	GT	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18245	115	GA	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18261	26	GA	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18268	88	CT	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299f	107	CA	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299e	101	AG	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299d	77	GA	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG
WI-18299c	67	TG	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTT T/GIATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCTG CAG

[illegible]

EST5	93 A ---				CTGTGGGGAGGAAACAAATTTGGTATATTACATAATGGAACCTCTTCAGAAATAAGAAAGGAA CAAACTCACTGAATCACACAACTGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTTCA TAAGAATACACAGTACAT
EST6	48 C ---				TTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A ---				GGACAGGACCTCTATTCGCCCTGGTGCAGCAGCGGCTGATGGACTGAGGCCAGGGGATCTGGGOC CTCTCTCAGGGCGTCCAGGACCCAGAGCTGTTCTGCTTTGAGTTCCCTAGAGCTGTGGGCCA GATAGCTGTTCTGAGTTGCAAGCAGGATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 GT ---				TCCTCATTGTTGGGATGATGAGAAAGATGTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 CG ---				CCAAAGTCTCCTGTGCTCATAAAGAAATTTTGGGATGGAGAGAAATCCAGACCATCTTGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCAACATTTTGAATCCACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACTTTACTTTCACGGTGGTTTGTGTTTCTTAT
WI- 18985a	105 CT ---				GCCAGAGCTGAAGTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGAAATATCTTG/AJCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-18746	114 GA ---				CCGTGTTCCACACACACAATGGCAAGCATAGTGGCTGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAAACCAAGAAACCGACGACAAA TCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACCGGTGATATCTTTGAG GGTGACAAGGC/GJCTCTTCAACAGTTCATACCACTGCTTTGCTCTAG
WI-19112j	212 GA ---				TGGTGGCTGGCTAGTGTCTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATCTTAGATCATGT CTCAATGGAAACACTCTTCTTCTAGCCCTTACTTGAATCTTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGTATTAACTGAATTTTC TTTTAAGCTAACAAAGATCATAAATTTTTC/NCJATGATTAGCCGTGTAAC
WI-19092	232 AC ---				CCCATTTATTATAGGCCAGTGTCTCAAAGAGTAGAGGAGGTCTACTGGTCTTCACTCTTCA GTCTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGAGTCCAGGACCGGACGCCACTG TCTTCATGCAGGAACACAGTGCAGATCCACAGCTC/GJCTCTTTCATCTTGGTTTGCCACA
WI-19057i	175 GA ---				

WI-20103	168	C T	---			TGGGAC TTC AACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTGCACATATACATATGCACACCTTTGGAGTGGCAACATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAAAGACAGAAATGG[A/G]TGAATAAGTACCCCCCA CATATACAAGAAAGTAGCATACTTACCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b						TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTTGA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAAATGAAGGCAGTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCCTTGGAACTTCGACCCGACTGTCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAG T[C/T]GAAAAACCAAGTGGAGCTGCTTTCCAAAGATGTTCTGTCTTCAAAATAGGAATTCATG TTATTCTTCTTGGCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTATTGTCATCCAAACACGCTCTTGACAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGTCTTTAAGTGAAAAATGGTCGAGAAAGAGGCAC[C/G]A[GGAAGCCG TCCTGGGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTCTTTTGCCCTTTTGCAACC

WI-20146	31 T C ---	---	TGAGTCTTCTGTATTGAGCAGTTAGC[T/C]CATTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTATCCCCCATCATTAAGTAAAGCCCTCATTGTAATGTGTGAATTCATACAGGC
WI-18922	74 G A ---	---	TAGGAATTGGTTTACGCGCTGAGGCAATTAGACACTTTTGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAAGTTCTC
WI-18763b	53 A G ---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[AGT]ATTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTTGTTTGCCAA
WI-18763a	38 A G ---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGG[A/G]TGACGATGATGTGAATTTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTTGTTTGCCAA
WI-18771b	75 G A ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGATGCCTAGAGATGTTGGG AACAGAA[G/A]AATAAAGTGAAGTTAAGGGGAGCTTAAACTGCTGAATTCACCTGTGA
WI-18771a	57 A G ---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGATGCCTAG[AG]AGATGTT GGGAACAGAAAGAAATAAAGTGAAGTTAAGGGGAGCTTAAACTGCTGAATTCACCTGTGA
WI-18820	70 T C ---	---	GGGAAAAATTTGAGACGCAATACCAATACCTAGGATTTGGTCTTGGTGTGTTGATGAAATTTCTGAG GCC[T/C]TGAATTTAAATCTTTTCAATTTGATGATTTCCCTTTTAGGTATATTGGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACATTTGCCAATGTAC[CT]ATCGGGTTTGGTTT TCTTGATATTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	GTGTGTCCTCAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA[CT]ACACAAACAAACGTAAGTTTCAATTTGGCAAAAAATTGA GC
WI-19970b	167 G A ---	---	TATAAGCCGAGTCAACGAGCAGCGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCCAGTTCTCTCACTGCGGGGACC AGCAAAAGGCCCTTCTCACTGGTTGGTCAAAAG[G/A]TAGTCACTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCTTAAACAGAGA
WI-19970a	126 T C ---	---	TATAAGCCGAGTCAACGAGCAGCGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCCTGCCACCC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCCAGTTCTCTCACTGCGGGG ACCAGAAAGGCCCTTCTCACTGGTTGGTCAAAAGGTAAGTCACTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAAACAGAAATCTTTTAAACGACTGACCTTCTTAAACAGAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTTCTC TTGGGCTCTAGGCTCTGGAGATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAAAT/ GACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCTGACATTCACGGCAGAGGCTGCTGCAGCCTCC/CJGCTGGCTG TGCATATCCCTCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTCAGTGGGTT CTCTGGGCTCTAGGCTCTGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTAGAACCTCTATTTAAT/CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAACAAA AATGCCAGAGGATAATATTGATCTCCACATCTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/CJGTTTAAATTAATTCACAATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCTTAAATAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAAGTGAAGGATTGGATGTTTCATAATACATAA GTTCTCTGTAATTACAACATAATATTATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTATAGATTTATGTCCCATGTGGGATGAGTTTTTAATGCCACAAGACATAATTTA AAATAAATAACCTTTGGGAAAGGTGTAA/CJACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCACGAACTGGAATAGCCTTCGAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTGACCTTGTATTCAGATTAACTGTTCCC CTTGGTATTGTTAATACCTGTACATACTTTGAGTTCAAC/CJCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAAGACAACTGTGTGGCTTG

WI-19042	193 A C ---	---	---	TTTGTAGTGTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAAGGTGAACCTTTGTGCTTCAAGGACATGGTGAGAGTCCACACAG ACACAATTTATCTGCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTTAACTATCTCTTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAAAACACTACAGGTGTTGAATGGTTAAAA TGTAGGCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGAGACAGCTATTTCGCACGTATTAAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAATGCTAAATGCTAATTTATCACTGGCATGTTGACT
WI-18851	90 T A ---	---	---	GCTTCAATTGGCGATTGATTGAGTGCACCAATGTAACAGGTTGGTAGTTGTTACTCAITTTGAAT ATACCTTTTCTTATTGTTATCTT[A/G]TAATATAGGATCCTGGAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGCTGGAATCTGTCTAGGAGCCCTCTCTCGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGCTGGAATCTGTCTAGGAGCCCTCTCTCGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGTCTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCTGAAATCGGGACAAAGGGTTTATCTAATAAGTGCTCTCCATCACGTTG CTAGCTTACCACACTTCCCTCTGATTGGGTGAGGAGCTGGCATCTCTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	---	TGGAATTCCTTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG[G/C]TAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATTCCTCCCTATCTTTGCCACCC TCATGCTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTCTCTGCATGTTACCAGAGCGCTTCTGTCCTAGCCAGCCCTGTATGACCCGCGCAATA TCCCAAGCTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACAC[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTCTCTGCATGTTACCAGAGCGCTTCTGTCCTAGCCAGC[A/C]CTGTATGACCGCGCAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGTGAAGTGTGTTGGAGGGATTTGTACACTGCATTGCTGGGCTGTGTTCTT/ CJGGGCTCTTCTGGACCTTGACCCGTGGATACCAGGCCATGTGCCATGTTATTTGGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCGTGTGGCTTATGTACCCAAACAGAGGGGTCTGTGAGAAGTCTGGCTGGGATGGCCCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAGAGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCTGTGGCCACCAGGCACCTACGGCTTCTCTCTCC AGATGTGCTTTGGCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAAATTTTGTATGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGATGTATACAGAGGTTCTCTCAAGC/AJCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAAATTTTGTATGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGATGTATACAGAGGTTCTCTCAAGC/AJCTCAACACTATTGAC TTTTGGGCTGGATGTTCTCTGTGTGGGGTTGTCTGTGGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTATTTCTTCTGTGTAGAGACTGGGCAAGCTTTGGCTAAGGACACCCGCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAACCAAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCCG/AJCTACCACCTCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTATCTGGTAGCTGTGTATCTAGGGATTGCACCTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAACCAAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTTGAACAAGGAAGTGGCATAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTATCTGGTAGCTGTGTATCTAGGGATTGCACCTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTATCTGTCTGAGGGTTCTGTTCACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAGCCCAAGCTCTTAGAGGCTCCA[G/A]TCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTTCAGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGACACTAGGCCATCTTCTCCCAATGTCCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCATTCAGAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAGCCCTTAGTATTTGCTGACATCTGCCCTTATCCTGTCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGGTGGCAGCCAGCCTTGAGAGCTCTTGTAGAAC GGAAGGAAGGGGGTCAAT[G/A]GGGTATGGCTCTGTGGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTTAAATGAATACCTTTGTTTGTGTCATGTTCAAAAAGAGATTAAT ATTTTGTAGCTGCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTAGGTTAATAATAA GGCTATTGTCCACCCACTCTTCGGCATTTGCTGCAATATCTCGGCTCAAGTGGAGGCCACGTG GGAACAAGGCTCAGAAAACAAGGACATGCAGCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---				TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/A/GJGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTTACAGCTGAGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---				TGGCCTCAATGACTGGTACATTGGAGAAAGCTG/AJTGACAGCAGCATCCTTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACACAGCAGAGTTACAGCTGAGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---				CTTCCTCTGTTGGCTTTCGATTGTGCGATTGGAAAAACACATTGGAAGAGGGACTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCTAGGAAGTCAGTGGAGCCCTTGAICTGAIC/GJAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-20512c	59 T G ---				CTTCCTCTGTTGGCTTTCGATTGTGCGATTGGAAAAACACATTGGAAGAGGGACTT/GJTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCTAGGAAGTCAGTGGAGCCCTTGAICTGACAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-19599	230 C G ---				GGGCTTAAATTCCTCTGTTGGGACTGGTCTCCAGTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGTCATGTTGGCTCACAGTAACCAACACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---				TGTTTGAATAAAAATTTCCATGGTCTTAAATGAACTGTATGTTACTTCTTTTAGAATATCCTTTT TTCATTAAATAAT/CJCTAAACCACTCTATGTGTTCAACCTTCTGTTTAAACACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGGCGAAATTGGTCTTGTTTGGAAAGCTCTC CAGGGTGTTCCTCAGAA
WI-19909a	29 T C ---				CCAGAAATAAGCCTGAATATCTCTT/CJTTAAAAATAATTTTCCTCTTTGCTCTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG TTTTTTCCTTATACCTTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---				TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGCATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTTGTTAGCAGGA GGCAGGAAAGTGATCTGGGCTCTGCGCAGCAAAAGCGTGTTAAATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTTTC/CJATGTCTCCAGTGAGCTGTGGCAAGTCT

WI-20113	60 T C ...	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAGCAAATTACACACAAATTAGGAGGAATTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATTCATTCCATAAACAGGTAGATAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ...	---	TGATGGCAAAGTACAAAGGCTCTGAAGACACAGAGTAACAACAGCAGCGCAGTGCAGCGTGTGGC CACTTCCACCAGGCAGAACACTTGACTTCATTAGGCAAA[G/C]CTTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ...	---	CCTGCAATCACAAAGTGGAAGTGTGATATTTTGAATCATACTTGATTAAACCACTTCAGAAA TTCTAT/CJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ...	---	CTGGATTTTAATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGGCAAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJ/AGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ...	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCTATGGCGGTGA/C/TGCTTCTCAGGCTCATATGGATGTCCT CGAGGTGCACAGGGAAGTCTGCTGCTTGTAGAAAGCTTCOC
WI-19348b	98 G A ...	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCTATGGC[G/A]GTGACGTCCTTCTCCAGGCTCATATGGATGTCCT CGAGGTGCACAGGGAAGTCTGCTGCTTGTAGAAAGCTTCOC
WI-19635	98 A T ...	---	ATTAGTTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTAT/GJ/ATCTTATTGTAGCACGGCTGTGAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCACGTCGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCGCTT T
WI-19641a	46 A G ...	---	TCCAAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCAGTAG/GJ/TATTATAGTCTCATGTTT TTAATTTATGAATAACGTCGTGATTCATTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCACCCACCTTGG
WI-19642b	52 C A ...	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTC/AJGGGTAACCCAG GACTATTGCATGAGCATTCITTAATACGTATTTGTAGTGACACAAAGTTTCATGCTATTA
WI-19673b	180 C T ...	---	TCTGCCATGATCAGATTGTGATGAMGACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCGCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCAGCTGTAATCTAATAGT GAAAGGCCAAATGATGTCTCAGTATCAGTGTGAAACATTTTTC/TGCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTCAAGGTCCACACAGTCAAAAAACACAGCCC

WI-19673a	35	GA	---	---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACCTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT AGTGAAAAGGCAATGATGCTCAGTATCACTGTGAACAACATTTTCCCTTGGACCACTGTAAGAA TCTTGAGGAGCCTGAAGGCTCAAGGTCACACGCTCAAAAAACACAGGOC
WI-19724	35	AG	---	---	---	TTTATTGGAAACAAAGGATTGTAATTTGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACAGAGATTTGGTTTTCTCTT
WI-19307	196	TC	---	---	---	TCCTCCTCCCCAACTAGATGGTATTGATCCTCTGCCCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCCTTATGAGAAATGGTGGCTTGGGATGGAGTGACATCCCTTGTCTGT GGTGAATCTGCAAGAAAGAACACAGCAATGTATCCATAGAGCCCTTTAAAGAGACCCGTC/TGG AAATGGCCATGGTCTAATTTGGTGTGAATAAATAACCTCTTTGGCTG
WI-19269	85	AT	---	---	---	CTTCCCTCATCCCTCTCCACCACACCATCCCGGAACAGTCTCCAGGATTCCTGCCACCTGGC CATTTGGAGTGTCTC[A]TJTTGGTAGCAATGTGAAACACACAGGGCCTTTGTGGAGAAAATGG AGGGGTTGAGGAGTCCAGGAGGGCTTATTGAGGGCCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGGTAGGCA
WI-19946	122	CT	---	---	---	CAATGGACTGAATGAGTGCCTGGTGGGGGGGACACACACCTTCAATACACGTCGAAGGTGG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTAGCCTGAGACGACAGAGAGGTCT/JTCTTCCCTG ACCCAGAGGCACTCACGAGCCAGGCTCTGGTTTTTCAAACTGCATTTAACCTGGCCAGAGAGTTCAC CGTAGGCATCTTTAATAAATACTCACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	GA	---	---	---	CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTTTAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTAGGGCCAAAGTTTGGATCTGTCTGGACCT CAATGT[G]A/CTCTCGGAGAACGACCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCAAACAGAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACAG
WI-19076	40	GA	---	---	---	TTGGTTGGTACTTGTCTGGAAAAAAGCAGTTTTAA[G]GTATTCAAAATACCTTTTAAAAA GTATTCAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTTGAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCATTCCTCAATCTATCTGGCTCCTGAAAAACTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATAAGGATTTCTTTTATCTT
WI-20218	26	TC	---	---	---	CCACACACTCTGGTTTTATAAGCTA/CJAGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAATAACATAAATGGAGGGGAACAGTGGGATGCAGAAAGAAATGACAACAGCCACATGTGCCCA GTCAAATACTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	TG	---	---	---	CAACCTTTTGGACAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATCATAATTG GGAAATCCTCTTTTAAATATCTCCAGGCTTGATTGGGAGGGGCTGGGCTTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT/GJCCAGAGAAAGCGGGGAAGCCCAAGCTCTCCAGCATAGCCACTGTGG GTGGGCTTCACTTCTGTCCAGTCTCTCATGCTGGGACTTGCTTTCGGGG

WI-20361a	192	GA ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCAAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAATCTGATGTCGAGAGTTACACTCTGCACCTCCAAGCTA CAACAGTGCACAGCTGAGAGTTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACACGAGACAAATGGGTCTCTACAGTAGGCCCC
	75	AG ---	---	GAGCCAAACCCAAAACAAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATT[AG]TCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTCA AATTCATCTTTCTCAAAATTTAAATTTTAAATCCCAAAGGTCCTATGAATCTCTCAAAAATA AACTGCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20572	133	GA ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACCTTTTAAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAGG
	79	AG ---	---	TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTG CTGTACTTCAG[AG]TTTAAATCTGGGAATGAGCATGACGAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCTTCAOCAGACTAT CCAGAAAGCCATTCATGGGGTATTGGTCTGCATACGTGAGACACTGAGCT
WI-19765	57	TC ---	---	TTCTTGCCAAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGATACCTTGCTCTCA/T[C]ATGTATCT TGCTCGTCTGCTTTTAGGTAGCAAGGTGATGAATACTTTTAAGTTTTGTTGTTCTTTTCTCGT GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGTCAAATTTACAAAATTGCCATGGAACTGAGC AAAGGCCACGTGGGATAAAATCACTCACCATCGACGCCACCAGTATT
	239	AG ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGTGGTCCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCTTCAC[TAG]GTTCTTTTA
WI-19066g	184	CT ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGTGGTCCCTGTAGCTGAATTAATCTTCCATATTC/TGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTCTTTTA
	148	TC ---	---	TGACAAGGGAGAGAGGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGTGGTCCCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTCTTTTA

WI-19066e	147 GC ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACCTGG CATATGTTCTTGG[G]CTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100 GA ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87 CT ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066a	72 CT ---	---	TGACAGGGAGAGAGGGAATCTACTATTGCAAGGAAATCCTCATTAAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAACCTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105 GC ---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGTGAAAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTGT[G]CTTAAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAAGATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTATGTTTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCCCTCTCTCTCCAGCCCTGCCGTGCATGTCACCCCTTGGTCTTTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 CT ---	---	TTCCCCAGGGTCTGTATTGCAGCTAAGCTCAATGT[G]TATTTAACTCTAGTTGCTTGTCTTTG GTCCTTCTCCAATGATGCTTACTACAGAAAGCAATCAGACACAAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGTGCAAAACCGCAACCTGTAACCTGCTTAAATGGCATGACAAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 AG ---	---	GAAAGCCAGAGATTAGCCCGCATTCGCGATCTGTCAACCAAGGACAGAAATJGCGATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 AT ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC[G]ATGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGCTAGGCTGGACACAGGATTCAGAAAGACACCCAGGCTGCACA GAAAGCCAGATGGACCTGAGTGTGCGTGCAGCCCTTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA
WI-18987	35 GA ---	---	

WI-18919	26	CT	---			TGGATGAAACACACAGGGATTCCGGAC/TJGCCAGACCCCAATTTTACTTCACCTTTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACCTTTGGCCATACACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64	GA	---			CTTCTGCTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	GC	---			CTTCTGCTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTOG CTGGAGTTCAAGCTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	TG	---			CTTCTGCTCAAGGCTTTGGACAT/TGCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTOG CTGGAGTTCAAGCTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	GA	---			TCAGAAGCAGACATGGCATCTGTTCTTCTGCTTGTGTTGTTGTGTAOCTTTCACGAGACCTGAATT TTAGAAATGCCAGTGTGCGCAGAGTGAGTGAGTGAATTTCTCCTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTTCATAAACATATCAACC[A/GA]TAGCATTAAOCCATTTTATTTCTGCTCCTT AGTGCTGAAGATGCTCACCAAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	48	TA	---			CCAGTTGCATCCATGTTTGTATTTCTGATGAGACTAGAGTGACAGT[A/G]TTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATATGAGATGGCTATGGAAATGCAGCTGC ATAATTACACATTATCAAGTCTCTTACAATTTATTTCCGACGATGTCAGCTAAGTAGACCCA ATGGGAGAGAAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210	GC	---			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTCTTCCCATTTATGGGCATGAAATATGGTTTAGAATAAGGAACAAGCATTATT CCTTGGCAACAGCCTCACTAAGAGGCTTTTGTGCTGAGTCAAGCAAACTTGCTGCTCTGCC CTTGGAG[G/C]TGCAITTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	TC	---			TTGAAATCCAGTCTCTGCCCCCAGGAGGGTCTGTACCATAGATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTCTTGTATTCTGAACTGGAACCTGAACAGTTTGGCTTTCTCTCTAGTCACC AAGCATACTT/CJTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	TC	---			GTCTCCACAGAGTCTCTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGGGTG CACGGTGAGAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCCTTCTCAATACAGCCTC/G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20	GA	---			CAGTTACCCTGCTTGGCTC[G/A]AAAGTGTCAATTTTGTAAATTTTAGTATTAACTCTGTAAAGT GTCTGTAGGTAGCTTTTATATTATATAAGGACAGACCAAAAATCAOCTATCAAGGCTTCAAAAAC TTGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAAC GCTTTTGGCCATATAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGGTGGCACTTGGACTCTGAGGGTTGGGTGTGGAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTGACCGGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACTTACCCCTTTTCATAGGGGAAGAGTGTACACACTCTGGCTATCTCAGGGGGAATGGGGAAG AATCTTCAAGGGCAAGAACTCGTGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTACGCTTGCTGACCTCCAGCCTTCTAAGG CTAGCCACACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATATTCATTATCATAGCCAA ACAGGAGACCCCTTTGACAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTTCTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGCTGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGGCACCTGGACGTGTGACGATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCCCGGAGATCTAGCATCTCTGAAATCCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGGTGGCAGACAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGGCACCTGGACGTGTGACGATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGCCCGGAGATCTAGCATCTCTGAAATCCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAGAACCTAAACATGAAGGAAAGGGTGCT CATCCAGCAACCTGTCTGTGGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTGCTCAGCTCTCCTGCTGTGATGTGGAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTCCTCCTCAGTCCCCCAGATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATGTTCAACAATGGTGGAA[G/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTTCCCTAACTCACCAGTTTAGTTTGGGATGATTTGATTTCTGTGTTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTCTGTAGGTGAGTGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCTTCCCTTAAAGGACTCTGCGGAAC[C/T]TTTACACACCTCTTCTCAGGGAC GGGCAGGTGTGTGTGTGACACTGAGTGTCCAGAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTACAGGAACAACACCTTGCCTTGAATTTACACAGTGAAGTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	CT	---			CTCCTGTTCTGACCTGACAGGGGTGACACAGCCCTTTACACACTCTGTCTCCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCOCAGCAAGGGGTGACGCCAGGGGTGAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTATCCACTTGCTCCTCCTCTACCCTCGGCACCCCTGGGTGGAAAGGG
WI-19134a	162	TC	---			CTCCTGTTCTGACCTGACAGGGGTGACACAGCCCTTTACACACTCTGTCTCCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCOCAGCAAGGGGTGACGCCAGGGGTGAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGCTCCTCCTCTACCCTCGGCACCCCTGGGTGGAA
WI-19224	112	CT	---			GGTTTACCAGTCTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTCATAATCCAGCAGGCCAGAAAGACTTCC AGGGAACCTCAATTCAGGAGGTGAAATGATGATGACTCTCCAAAGATGAAAA
WI-19201	179	TC	---			GCAGCTCCTAAGGACCACCTGGCCATTAGCTCTTGCTTTTGATGGCATTCTCTTCCACCTTGCTTCTC CTTTGCTCCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTCTGTTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAGGTGACACTCCATGCTGCTGGCTTGGCCTCAA
WI-19034	45	TC	---			GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGAAATCTACTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGCATATAAAATTTTTTG CTAGCCCATGATCAATCGACTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTGCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	CG	---			TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTTCTGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTCTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAAGTCTAGAATCTCTGTAAGTTTGAAGTCAAGGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTTGAGTCCCATAGAACAGAAATGGG
WI-18548b	65	AG	---			AAAGGAGGGAGAAATCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCCTCACTGGGGAA[AV GJAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	GA	---			AAAGGAGGGAGAAATCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCCTCACTGGGG[G/AJA AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	TC	---			GGCAGCAGCTTTTTTAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTTGAAGTCCACAATTTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121	CT	---			CAGAGGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAAGGAGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCGCAGGACAGAGGGGGCGCTTGGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C A	---			ACAAAGAAATGGAAATAGTTTGGAAAACCTTATCTGCATGACAAAGTAATCCCGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---			TTATTGGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTCAGAAACCTTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGTATTTGTGTGACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCACAT/C]GCCAAATCCCTCTTCTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117	C A	---			CAATGGGTGGAGTGAGTATAAACGCATATTGAGAACAAAGACGGCCTCTGCGCNCCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTGGGTGGTTCCTCAG
WI-18295	40	C T	---			ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCTCTCCAAGGATGATGTTTAATGAATCCCTTNCCTTAGCTTCATTTCTCATATGCCAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ C]GAGTAATTAACAACATAATTTTANATGACAGTGAATTAATAACGCTCGGGTAAGCCAGAG GGGAGAGGGGCTTCTCA
WI-22585	56	A G	---			TTATTTTAAATTTGCATCTGAGATAATAAAATTTATCTGACAAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---			GGCTGTGGAGTAACAGAACTTGATGGAAAAATGGC[A/G]TGTGTAGAAATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTGTCTTTGTCTCAGAGGCTCAGATGGATACGACGCACTTCCTTTTGAACCTTTTAT TTCTCGCAGGAAGA[A/G]GATCCAGCAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98	C T	---			GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCATTTAAATGGTAAATTCATGTTATGTGATTTTCACTCAATTAAGAAATGGAACATGT CTTATAATTGTAATTACATGAGANCAIATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACAGATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCACCTGCCCAACCAAAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTTGGAGGTTCATGACAGGATTAGTCTTCTGTGTTT/C]CTTGGT GCAAGTTGAACCAAGTGAATATGTACCAATTGCATCAGAGCATCTGTTCCCTGTCCAGATCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC[C]GGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTATTAAAGATGGCTGTTT[A/G]TAAAGTATAAAGCAGTTTGAGCAACACTGATTGGCATTTA TTGACTTCAGATGAAAAATCCTTACATGTGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCCTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTTAGAAT AT[A]ATAAATCTATATATATATATATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---	---	GCCTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTT[A]TAGAA CATATATAAATCTATATATATATATATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---	---	GCCTTCATTTCTGTCAACCCAC[C/G]CTGTCCACCAGTTATGTTGGCCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATATATATATATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGACATATTACAACACAG NTCCCAATGGTGAACCTGGTATTTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[C G/A]GTGAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAAGATAATAAT ACAGTAACACTACTTTTTATTCTTTGCTCTTTATCCCTTTTTCAGGTTGAT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCAATTTTAAAGAACTACTCTCAAC[A/G]AGTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATAATCTTTGTATTTATTCGAGGAAGAAATCT ATAAGATTGACTTACTACTATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAAATTAAGTGGTCTGG GAGATTGGATAGAT[C/G]CCTAACCTATCTCAATTTTAAAGTAAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGATTTGATGCAATGTCCCAACCAAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCATGTAACATACAAAGCATATTACCTCCCCCTTAAGTGACTCATATTTTC ATTACTGTGCTGTAGCTTTTAAAGGTTTAAAAATGTAGCATTAAGTGGTATTACTTTAGGGCA ACA[G/A]AATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	---	CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTCTCAAGGGTGGATATGTTGGATGCAGACTCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTGAAGGCTGTTTGTAAATGCTG
WI- 21778b	155 T C ---	---	---	AAAAATCCATAAATTTGAAACCCCAAGTTACAGAGAAAGTTCGTAACCTTTTATTGAATTATTGAC TCTGCCCGGTGCTGTTGGTGGCTTTCAACTCCAGTCTGTAATGCCCTGTGTAGTGGGTGCCAG GTCTGGGCTTCTGAGGTCCTGCTGAGAGGAGGGGAGGGTGGT
WI-20907	241 A C ---	---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGGGTACATGAGGGCAGTTGTTCTAGTACCCATTAGCCG ATGGCTCTTCAAGCCAATTACACTGGGAAACACACCCCTCACAGATGCCTATCCATTTGAGTTG ATACAGGTTTGTAGCTAGAACTAAAAACATTTTAA/CJAATTATCTA
WI- 21449b	222 C T ---	---	---	AACAGCAGCAGTCACITCCAAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAGANTTGAAGGTACAAGAAATCAATCAAGCAGCACTGGAGGCGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAGAAAGTCCCACTGAGAGGCTCCACACCC AAATCATACCCCTCAGCTCCCA/C/TTGACAGAGCCAGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	---	GCCTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCGACTCCAGCTGGAACCTGOCCTC CCATCCCCCTTAGCGCTCTTGGCTTCCGGCTGATTTCTTGACAGCAGTCTGCGCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCGTGAAGAGAGATGTGGTCAAGGCTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	---	TTTGCTGTGGAATCCATGAGAGCGCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAAA/C/AJAAAAACAAAACAAAATACCA ACAGATCACCTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTCATGAAATTTCC CCTAAACCATAAACAAAACGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 22187a	110 C A ---	---	---	TTTGCTGTGGAATCCATGAGAGCGCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCTGGGCTGACCAATGGGTGATTACATTTAAACCAAA/C/AJAAAAACAAAACAAAATACCA AGAACAGATCACCTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTCATGAAATTTCC CCTAAACCATAAACAAAACGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG
WI- 21809b	146 G A ---	---	---	TCATGAATATGAGCCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTACAAGCTGTAA AACAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTCAAAG/GAJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAC/CJTGTCAGTCCGTTCCACAAGCTGT AAAAACAAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAAAGGAGCCCTGTA AAGGATGTTCAAGGAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	---	ACATTCGAGCCAGTITTTCCATATTCCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGCTTCA GGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCTAAGGCGAGGAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTACAGGGG TTTC/JGJTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/JCJTATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/JGJTTTCA TCATACAAGACAAGCACAAAAAGCACCCACCTGCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGG/JAATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAGCACAAAAAGCACCCACCTGCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	---	AGCCAACCTCAAGGCCAAAAAATTTCTTAATATAGTTATATGCGAGGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGATA/GJAGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	---	CTCTGAACCTAAAGGGCGGTGAAGGCGATGATTGGTTTGGCACACAGAGTGGATAACCAT/JACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 C T ---	---	---	TGTTTTTGAAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCATCCAAATGATTACTAGCAGTAGGAA GCCAAGCGGAANAGGACCCCGCGGCTTGCT/JGJGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

WI-21661	117 G C ---				GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCACAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACCTGTCCAGTGAAGCCGTTAAATTTTGCTCTTCAGCTATGAAG GA
WI-21980a	25 T C ---				TCAGTTAAACACATTATCAAGGAT/CJAGATTAAATTAATGTCAGGTGAGCATAAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAMGTGACTCAGGATAAGTTTATTATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---				TGCTTGATTAATGTGGTGTTACATTATCCTATTTACAGATGGAACAGAAAATACCAGCTTTTT AAA/GJTAGCAATATCTATTATATAATAATATTGAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTTCAGAGGGAGAAAACATTACCTCTAGAGCTAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A ---				TTGCTATAATTTCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAAACAGTAAACATACCTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACATAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCTGGGGCC AAAACCCACTGAACCTACCCACGCTGAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97 C T ---				GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAATAGCCGTGATGACGACCTTCGGCTACACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTGCAATGGACTATTGCCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGGGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 A C ---				GCCGTGAGGGTAGCGTATAATGAAAAGGTGTAATAGCCGTGATGACGACCTTCGGCTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTGCCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGGGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 G T ---				TTACCTTCCAAACAGGCCACCTTTGGAGAAAG[G/T]AAGAGATGCTATTATCAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCOCTCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 A G ---				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTGGGAGGGGCTC TGCATCCCCCTTCTCAGCACAGCACCATCTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCA CTTGCTCTTCTCACCAGGGTAAGAAATGCAGGTATTTCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGACAGACACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGBAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCGAGGGCTC TGCATCCCTTTCTCAGCAGCAGCACCATCTTACCCCTCCTGGAAAGCAGCATTGGAGCCTACACQ A/GCTTGTGCTTTTCTCACCAGGTAAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG
WI- 22683c	139 G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGAGGTGAGCCGCGCTCGCTAATCTTATTC CCAGTCTGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22683b	55 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGAGGTGAGCCGCGCTCTGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22683a	38 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACCTGCGCTGAGGTGAGCCGCGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGTAATCCGTGTGAATGTGGGT
WI- 22681a	52 T C ---	---	TCCTTTATCCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTGAGGGAGCCCTTGGGATT CCAACCTAACAAATAGTTTCTGTAATAATTA/GJTCTAGTCCATTAGATTGTGTAATGATCTAA ATGGNGTAACCATTTAATAATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTCAGTCTGAT/CJAGCACCAATTT CAAGTTTATGGCAAGGTATTTAACTCTCAGGCTCATTTCTCTTTGIAAAATTTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAATCAACTGAAATTTT
WI- 20258	157 G T ---	---	AATCCACACTTTCACGAGGGGACCAAGCTGCCATGTGCTCCAGGCTCACAGCAGCGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGTGTTCAG/GTCCGTTGACGAGGTGCTGGCTGGCAGCGGCGCTCTACAGA AGGAGGAGCGCAATTCACAGCCCTTTCACGTAGTTTCGGGGAAGTAOC
WI- 22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCACACTCTCCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCTG/ATCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCTGCGAAGCCATAGTTGGATGGGAGACTTTTCGGCAGAGGAAAT AGCAAGTGCAAGGGGCTGAGGGAGAAATGAACCTTGGCTTGTCTACAGGGGTGAAGGGCGCGGCT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGAGTGTAGAGATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACGTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAATG[A/G]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTGACCATTCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTACAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22806	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCCTCGTGTCTGAGCCCTCATCCACCCCTCCAAAGCCCTATGCCACACACACCGTGTCCACATT CCCCATCCTCCCTGTCTGCCCATCTCAAGTCCAAATTCOAAGCCAGAGCCCTGCCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTGAATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31 C T ---	---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGCTCCAACGGTGGCACA TCCTCATCTTTGTTATATACTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTGATTTTATTTATTTGTTTCTCCATTTCTCTGCAACCTTTTC[A/T]TTTGTATATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTTCCTGAGTTCCTGAACCTCTTTTAGAGG
WI-21186	95 G A ---	---	---	AGCGAGCATCAGAAATCACCCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCTTAAGTGTGCAG ATGCTGTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGATTGAAT
WI-21187a	94 A G ---	---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCAGTAATGCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTCATCACCTAGGGGAATGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---				TTTTCCACATACCAATGCACCTGTTTGATATAAACTATTCGTTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTATAACAAATAATTAATAATCTGTACTATTACTGCG TTAGTTTCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTTTCCATGTAAATAAAAGCTT AACACA
WI-19937d	186 G A ---				ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGTACATTTGGTGTCTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-19937c	185 C T ---				ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGTACATTTGGTGTCTTCCTCAGCAAGTC[C/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-21117b	227 C T ---				GAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACTGAAAATCTGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAATTTTCAGAGCCTTCAATACATTTCTGGGG TCCAATCACATCTCAGGTTCCAGCTCCTAGCTCCCAATATTTCTACAGTTCTGAAGANITAGCAGT CCTCTCATTTCTACAGTCTGATTT[C/T]TCTACTGAACTTGGGTGGGAG
WI-21122a	42 C T ---				TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA[C/T]TTAAGAGAACTCTGTTTTTCC TTATTCAAATGTCAAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACCTGGAATACT AAACAAATCTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---				CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACATTTCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---				AAGGAAACTGCATGGGTACAAAT[G/T]TCCAAATTCATACTTAACAAGGTGGGAAACGGGTCAATCT TGGCCTGCTCCAGAACAAAGGGCGGAGTCTATGCACCTCTG
WI-21059b	181 T C ---				GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATTTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTTC[C/T]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGTGACTATCCTTGCCCTAAT
WI-21059a	63 C T ---				GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATTTTCCCACTGAGCCTGG[C/T]T GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGTGACTATCCTTGCCCTAAT

WI-20442	37 T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGGTGAAGCAAGGGACAAAGGGGAGCAGGCGAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATT/CJCATTAC ATCAACGTTAAATTTGTCCGACAGTCTTTCATTGCTGATCATTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAATGAATATTACCTTGTGCTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTGTGACAGGGATCTTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACAGTTCCTCAACCCCAACAGCTTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTCTTTTAAACATGACCTTATTTATCTTTAACTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/GATGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGCAGGTTCTGTGGTTAAACATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188 A G ---				GGTGCAACTTGGAAATAATGGTTTAAACACAGGATAAGCATTAAAGGAAAAACACITTTCAATGTGTC TTCCATTGATGAATTTTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/AG/GAAGTGATTCT GAAGTGAACGACGCTCATGCTGCTGCAATGGGAACTCTGGGGAGAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGCGGTTTGATCCAGTGGGATNTGGCTTCCC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAAGCTGCCATCCTC AGTCAGGTCGAGTCCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTGGAGTCCCTAGCATAGCTCCCTCCCTCAAGAGGGCAAGGGGTCAGGGGCGAGGC AAAAATCCAGTCTGCTTCAACACGGAGACTGCCCTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCGAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCCCTGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTATGAGGG AGGAGGAGAGAGTTGACCAAA/C/GTCTACATGCATAGACAGTCTCTAAAGCGGTATCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTT/CJGGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTATGGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTCTAAAGCGGTATCTCAAAACATG A

WI-21627b	153 A G ---				GCATGAAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTGAGTACCTCATATGGAATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATATTAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATCTCTACAATAATAAGGGTTTAAAATGIGTTGCTTA
WI-21627a	106 A G ---				GCATGAAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTGAGTACCTC/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTTACATAATTTGTAGG GACAGTATACTAATCTCTACAATAATAAGGGTTTAAAATGIGTTGCTTA
WI-21399a	75 C T ---				GGATTTAGTCCCACTTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTT/CJTTCCACAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---				CGATGCTCTGTAAGATAGGAGGTTAATCTTTACATGGTGGTGCACAGACAAGACATCAAT C/GA/JTCTGTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAACAGATAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---				TTCTGGCATTCAAAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATGTATCTAAGTTTCACTTTTAAAGAACATTATAAGGTAATT AAACTCTAGGTGTACTTAT/CJATGGAACCTAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTAATAACATTGAGA
WI-21504	147 C T ---				TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGCAGCGGCCGTTGGCTCCAGCTGGGTTTCCOC AGATGCAACAAT/CJTGCGGTTCTGGCTTCTCCACTGGTGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---				CTGCACCAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCCCTCCACCTGGCCATGGTGGTGTT CTCTATGGACCGAGGCCCTGAACCGGGCAGGGAGGGGAGAGAAAC/GA/CACCTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---				TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGOCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCATTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGAGTGGCTCTTTGGAGAGGCA/GJ/AAAAGCCACAGCAGCAAC ACTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTTCCCTCCCTGAAG

WI-21475b	117	A T ---	---		TAGCCCTTCTGCCAATCTGGCAATNTGAGGCTGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGTAGGTGGGCTCCAAACCCAGGCTTCATCTTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGCTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTAGGAGCAAGACCCCTCCCGTTCCACCCCTATTTCCCTCCCTGAAG
WI-20893d	207	A G ---	---		TGTTTGTGTTCCAGCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGCGAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAAATCTTGTACGTAAGTTTCATCACCCTCC AGCGTCAGGCCCAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCAGJACATAACATTGGTAGAGTAAACAAACCAACCCACAGCCTAAATG
WI-20893c	179	T C ---	---		TGTTTGTGTTCCAGCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGCGAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAAATCTTGTACGTAAGTTTCATCACCCTCC AGCGTCAGGCCCAACCTTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAAACCAACCCACAGCCTAAATG
WI-18941c	71	C G ---	---		GAGCTCAAGGGAAGACCCCTTACCCAGATAGGGACTAATCTGGAGGGTGGAGGAAACAAAGGTGAAA GGTATC/GGGTCTGGTGAGACAAAGCAGGGGGCCCTGAGAACACAGAGCAAGGTGGGTTGGAG GGAGCACAGCAGGGTGACGGAAGGAGATGGGGGACATTTCCATTTCCAGTGCATGTCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGACAAAGCG
WI-21552b	166	C A ---	---		TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACCTTTGATTTTAAATGTA/C/AJAATTAAATTTATTGAAATTTAGTTACCCCC ATTGTCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21552a	66	G A ---	---		TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACCTTTGATTTTAAATGTAACAATTAATTTATTGAAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54	C G ---	---		TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATAATTTCTGTC/GJTAGAGAGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCACAGGTCGGGAAAGCAGCTCGTGGTGTGATCTGTC TCAGTGTGGAGGCTCTCCACTCGCCCCACAGGAGCCCTCGGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGG
WI-21513b	192	G A ---	---		CACATAGTTTCTCAAGAGAGGATGAACCTGAAACCTCCTTAAGGAGGACAAAGCACTTTCCATT ATTCTTAGTTTAGACCAGAACTTTAATTTTATATTCCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAAATAATTCACAGTATACCAAAACATTTTAAGATAAAGAGGAGGTAA[G/AJAGTAG TATCTCTACATACCACAGTATACAAATGATGCCTTCTCCTGCAGGTTTAGGAAC

WI-21514b	133	CT	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGC/C /TACAGGACTCCAAAGGACCTCAGAAAGGATTTAGCCAAATCTCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTGAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	AG	---			TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAG GCCACAGGACTCCAAAGGACCTCAGAAAGGATTTAGCCAAATCTCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTGAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	CG	---			ATGAACATGTTGCAGTGGGATGAAT/C/GTTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGATCAITCTACCTGTATGAGGGTACTT
WI-19576a	113	AG	---			TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGTAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC/GTCTAGTTCAGTGATTAGT CACAGAAATTAACAATCTGCCAGATGTACACAATTTGGTAAAAAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141	AC	---			ATACACAGGCCACAATTGCAGGATGGAAAGGCGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTACCAACCCAGAAAGTTCTTGGGGCATGTGATGGCGAGACACCCCTTTCCAA GGGAATA/C/CTACTACACTAAGCCTACACTGTACTGTGAGAGTGTGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTGAGANITTC/TAGGCCACAGCAT
WI-21574a	235	CT	---			AAACCCAGAAATTTAGGTACTTTGTATTATGAGGAACCTACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCCTGGAGGTGACAGCTCTCAGTGAACAGGCG TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCAGTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCTTCTGCTGTCAGGTGGGA
WI-21644c	151	TA	---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGTCTTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT/AJTTCAATCAAGATCCCATGGAAATGATGCAGITTAACATGTGTTCTCAGC TTGCCTACTGACCACCTTCTCTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	GA	---			TGCTTTAACCTCAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC/GA/JTTTTAACA AACCTCATTATGATCAGCTGTGCAATTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTAAGGAGGTT GGAACAGTACTACGGTCAATGGTATTTTGGCAGTTGGCTGTGTGGG
WI-21615b	151	CT	---			GACCGAGAAAAAAGTCAAGGCATATGATGTTGTGCAAGTATCAGATGACTATTTCAAGCTTATAGA GAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT CTTCACTGAGTATTATCTGAGGACACAATCGACGGATGAATCTATTTGANTATACCATAGGCC TATCTATATTTGGCCAAAGGGAAAGGIAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAATTAAGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTCTTTGGGAATTACAGGAACATAAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACAGCCTCTCCACTGCT TACTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAAAGCTAACCTGGCCCTCTTGTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAACCTGGGATGAGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTGAGTCTGTAAAGAAGGA CACTAAGGCACATGGCTGGTGTATCTTTCGTATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTCCCC ACAACTTCCTCTTCCAGGGGAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTGAGTCTGTAAAGA GGACATAAGGCACATGGCTGGTGTATCTTTCGTATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGTCTAGGTTTCCAGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTC CCACAACTTCTCTCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---	---	CAACCTAGTCACTCACTACTGATGCAAAATGATTTGGAGGTGCTTCTCCTAGCTTTACAATAAGNGG GACCTCTGACTGCACTAATCTCTCTGCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCACTACTGATGCAAAATGATTTGGAGGTGCTTCTCCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATAATTGTTCCAGCACCCTACTTACTGTATTTCTTCTTGGAGAAACCAGGNATTAAAG AAATCTGGTTTGAATTTCCATGATGCCTAATCTATGTTAAATCTTTTCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGGAGACTGAGATATGTTGCAGAAATTTATCTCTACCTC AGAGACAATTCATAGTTTATAATCTTTTCCAGGGTGTGCTTACTTGGGGGC
WI-20934a	72 T G ---	---	CCAAACATGCAACATAGTCTTCTTCTTAAAGTACATAGTAAGGTATGAAACAAATTTGTATTCA GAGAAATGTTCTAAGACAAATGTGCAAAATATTCAATGGCCTGGCCTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAGCCGGGAGACAGTAATAATACGTGCCCATGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATCAGCCGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTTGTCTCTTAAC CTCTCCAGGCAAGAAAGGAAAGTGCATATATGAATTCCTCAGAAATGGTGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAGAGGCTTGAATATATATGATGATAAATGGTAGCCCTTCTGGA AATAATTTTGTGTAATCTGTTTAAAGATTTTGTGATGCAATGTCCCA

WI-21961c	200 T G ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTTGCAATTCCTTTATTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCCAGGAGTATACACTGCACCATACCGGCTTTTATCCCTCGGCCCTTG/CJCTCCACTTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI-21961b	73 G A ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTTGCAATTCCTTTATTATTATTATTACTTTTATTTTTCQGAJTAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTTCTTTAGTGGCATTGTGTGATTTGGTGACCCATTACCCAGGAGTATACACTGCACCATACCGGCTTTTATCCCTCGGCCCTCTCCACTTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI-21956	26 T G ---	---	---	CCCACITGGGTCTCTTCAAGTGAATG/GJTCCITTCGTTCTAAAGCCCTTTAAATGAACCTTCCATTCTGTTCTGAACTTGCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTTCTTCTGAGGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCCGTTAACTCAGGGTAACTCCTATCTCTCCACCGGTAAACAGAGGGTTACATTATGGGGTCCAGGT
WI-21966	148 G A ---	---	---	CAACATACATTATGGCTGCCCTTTATTAAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTGTAGAAAGCATGAGTGAGGTGTGTGTGTGTGGCGCGCGCCGACGGCATGGCACTGAGGGGATTGCAATGGG/GAJAACAGGATAAAAGGTATAAAAGTGGTCCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCTCACAAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATACTGGTTTTGGTTACATGGATGAATTGCTAATGGTGAAGTCTGAGATTTTAGTGACCCATCACTGAGTAGTGACATTGTACCCAACTTGTAGGCCTTTTATCCCTACCTACCTCCACCTCCCCATTTTGAGTCTG/CJCATAGTCCATTATATCACTCTGTATGCCCTTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTAAGTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAAATGTGGTCAAGCAGTAAGGAACATAACA/T/CJGTACAGCACTTCAGCACAAAGCCCTGGGCACACAGCACTGCATGGAATACACAGGTAACATTTTAAACAGTGGGGACAAAAATTTAAGTACGTGGCCAGCTGTGGTTGCTCTGGTCAATTAAGACAAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACAATTTTGTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATGATACATATTACTGCAGATAAAACCATCAACAGAAA/GJTJATTAAATTAATGCATATTTTGAGGCTACTCT
WI-22082e	179 G A ---	---	---	CAGGACTTGGTTTGGTGTCCCACTGCACATAAATGTCCCTTTTGTGAGTTATGGTTGTGTGGGTTTTCCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTGCTTTATCCGGATGACGGAGGTACACGGGGGGCTCGCTCAGTTCGCCCGGAGGACGATTC/GAJCTGAAGTGGGACGAGTCTACTCTCCCCCACAGGAGCCACCGATTCAAAATCCTCTTTTGTGTCAACCTCT

WI-22082b	67 C T ...	---	CAGGACTTGTTGCTGCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATGGTTGTGTCG /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTTCGGCCGGAAGGAGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ...	---	AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAATAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCATATACAAATTAGGGGAAAAAACCCCTGG GCTTCT[AG]TAAACAAGTGAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTTCAGGTCCTTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ...	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAAATAATTTCTGAAGATAACAATT TGGACTTTAAAGCTC[G]ACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ...	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAAATAATTTCTGAAGATAACAATT TGGACTTTAAAGCTC[G]ACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ...	---	CAACAGATGCTTGAGCCAAAAAGCAAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCCTTAATCTGACTTGCTTTACTATCCTTT[G]CCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCTTCTAGTTTAAATGTCCTGCCCCCAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ...	---	TGACAGATCACACACATTTTGTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[AG]AGAGGCAAGTACAAAAATGTAAACC CCACCAAAGTGCTGTAATGAAATGCAAA[AA]AGGCTTCATTGTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ...	---	CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTTCACATCTCTCTGCCAGTTAAACGTGCCGTGG CT[C]G[CA]AATACACACCAAAGCCAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ...	---	AATGAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGTATCTCCATGAATTAAGCTGTGTGTGCTCACTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[G]AAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI-21079a	50 GA ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATCAACTGTGTGA/ICGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTGATTCTCCATGAAATTAAGAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 TG ---	---	TCTGTAGATTTAGCCATGCOATATATTAACCTTTAAGGAAAGT/GTJTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAATAATTTGGTTGCAATTTCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCACCTGACTAAGGTTTTTA
WI-219141	79 AG ---	---	TGGAGTTAAGTGGGGCTGCTATTTCCCAAGAGGACTCGGAAGATGTTGATTCAGGGGCAGAGT GAGGGCAGAC/GJGGATGAGGCTCTCTGTAAAGTCAACAGACGCTCAGAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCTCACAGAGAGAGCTCAGTGCATTGACCCACACCCACCACCTCAAC CAGCACACAGGCACACGCGAGGGCACACGGCACACACGNTGCATCAACACGC
WI-18916b	42 CT ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAGC/TJGGCTTCCACACTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCACTACTGCACTGGACACAGCCTCAAC AATGCCACCTTCATA
WI-18916a	35 GC ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAGC/GCCTCAGCCGGCTTCCACTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCACTACTGCACTGGACACAGCCTCAAC AATGCCACCTTCATA
WI-19828c	200 AG ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCTGTAGCTAGTCCAGGNTCTTGCCCCAAATCTGGGTCTCCCCAAG CCCATGCTCTTCCACTTCTACAACTTTACTTCTCTGACCTCACCACCACCCCAAAATAG CTTTTAACTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 CT ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCAGCCCTGGCCCTGCTCTGCTGCTGCATGCCACCTC ATATCCACCCCATCCAGCCTCTGCCCGACACCCAGGCTCCCTGCTCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACCCACAGCATCT
WI-19860	51 CG ---	---	TTGACCTAAGCCTAGCATAAATAGCTAAGTAGAATGTTTCCAAAGATG/C/GJCTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTGCCATTCAACCCATAAATGGTGGGATCTACCTCCCT CCTTGCAAATTTAGCTGGNCCCTTGATCCTGTCTAAGGATCTGAAGCC
WI-19880h	80 CT ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAAGGCAAG AGGAGTGAGGGG/CJTAGCAGCATTTATTCCTCTTTCACCTCCTGTTAGCTTTGGTAGTGGCTGAT TTCCTACTGATAGTCTTGCCACAGTCGTAACCTATTCG

WI-19891c	172 C G ---				TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTCGTTGGTGCCCTCCCTCCCCCGG ACTCCTCTGTCTGGGAAACGTGGCTTGNCTCCACACAGCTGTAGATGACAGCTCTCCTCAAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTCQ/GJGCTTCOCGGGGGTGGGGCGTGTCTGTGT CAGCGAGGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---				GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCAACGGCTGTACATTACCTTAGGCTGACCAAT TCCCTTGGGGGGC/TJGCAAACTGCTTTGAGGAAATNTCCACAGGAGGAATAAACTAGAAAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGTGGCAGAAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTGTCTGTCAGTCCAGAGAGAGACTTCTC
WI-20270b	91 T G ---				AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCAT/GJACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGGA
WI-20270a	53 G A ---				AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCG/GJATCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGGA
WI-20622	130 T C ---				CCACTTTCAATATTTTACAAATGCTCAGCGAGCAATATGAAAAGCTTCAACACTTTCCTTTGTGA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/GJ TACTAATTTTATGATGTTACTCATATTTTATTCATATACITTTAATGACATCATTGCCCAATACATA CATTATTTCTNTAAGTTTATTTTACAATAAGCCCAACATCTGTCATGCAG
WI-20768b	190 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCCTGGAAAGGAGGGCTAACAGGACCTCTGCCTGCCTGC TCAGGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATCTGTATATACCACTCTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAAAGNTCAGCACACATACTGCTGGGA/CJTCAGGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCCTGGAAAGGAGGGCTAACAGGACCTCTGCCTGCCTGC TCA/CJTGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATCTGTATATACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAAAGNTCAGCACACATACTGCTGGGACCAAGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---				TGTTTGCTTTGTCCAGGTACTCTACTGCTTTACATAAATATCTCATCTGTCTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACTAAATAAGGATATTTGTTGGTCACTCTTTAAAGAAA TGTCCTTAACATACCAAG/ATJAGTGGAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTTATGGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCTTA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCACTGGCACAACCACTCTGCGGTGACAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTTNCITTTATGTGAATAGAAATGGCAGTGAAGTGCCTATG AACTGAGGCGAGGAATGGCATGGCGCTGCGGTACAGCCTGGACGTTGTCTTCCAAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGATCATAGAAAAAACCCCTCAGCCAGAGTAGGACATTGTGATCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTGT/CJTTCATTTGCAAAATAAAACCCA GACCGGTCTATCTTCAGTTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGATGATTTATCATGCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GAGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCCTCTAAGCACOG GCCAGTAGTGGGAATGCCACATGCAATGGGTAGTGGGATCTGGGGGGGTGAGGACCTGTCTTTT [C/JT]TCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGCCCCCTTNNATTTCTCTCCCTCTATTCC CCCTCTTCCCAAATGTCTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCATTGCTCAGTACCAGAG/GJGTTTGAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGCAACCAAAATGGCAGCTGGGCTAAGGCATATTAAACAAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCTCTCTCTCAGCAAGGCAAGGATTGGT/CJCTTGTGTTTCTG AACAGGGCCCGAGGCGCAAGGCATGCCATCACTGACGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAAATTAAGTCAAGATAAAGGGGCAACTCTTTAAT/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCCTCACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTTGGCTGTAAGTCG/JC/GATCAGGTGCTCTCCACCACAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGGNTCGCTTCCAGGCAGACGCCAGTGCCT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGCAACGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTTCTGTGTTTCGTTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAAT/CJTGGA ATCTGCATGATTAAATAACATTAAAGTTTCATAAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATTCACATTCTCCTCCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCCCACATTGATCTTAGTTAACAGTCTTGTTAGTTCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCACAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT GCTCTCCACACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCTACCCCCAGCAGCTGTCTAGTGCACIT
WI-21763a	135 T C ---	---	GA CATACCCCTTTAGGTGCCCCACATTGATCTTAGTTAACAGTCTTGTTAGTTCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGACCCACAGATACTTCCAAGTGGAGCCAGCCCTCAGACTGTTCTCAGTCACT T/C]GCTCTCCACACAGCTGATTACAGACATTGCCTGTGCTTCTACCCCCAGCAGCTGTCTAGTGCACIT
WI-22440	64 A C ---	---	GA CAGTCCATTTGAGTCCCCAGTCGAGGGTGCACTTCTCCTTTATCTTGCTTAAGCCACTTGGGT[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTT[C/G]GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAAGGCACCTGAACA CAGTCAGGCTCTCTAAACACTGGCAGGACCTCCCCACAGCC[A/G]CCCCACAGGGTCTCTGTT TCCCAAGCTCTGATGGATTTCAGGCAAGACCTTCACACATTACCCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAAOCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAAGTCTCATGGACTTCTTCTAAG[C/G]TGTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAAACAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTTCAAACTATTGACTATACAGAG TCTTCAATTTCCAAAACAGTTAATAGTAACTTGGTGGCACATACACATGCAATTTGAATAGTCTGTAT TATTGAGTAACTAAAT[C/JAGGNTCCCTGGCATCTCTTCACA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGTTATTATGGGGTCTCTGCCCTCCTGGCTGTGTATG[C/T] GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGAGGCACTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATAGTGGTTATTATGGGGTCTCTGCCCTCCTGGCTGTGTATG GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCOCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCCGCTGGCCCGAGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCOCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCGCCAGAACCTG[C/G]AGTGTCTC TTTGACGGGCGCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGGT

[illegible]

stSG1019	136 GA ---			GGACAATACTACCTAAGGACAAAATACTATTATTAACAAAAAGTCTTCTAGTGTATATTGGTAAACACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTCCATCTATACAAAACITTTTACTG[A]TTTGAAAACCTGAGATTTAAGTTGCAAACCT
3				
stSG1020	143 GT ---			AAGCTAACTTAGGTGAATGGTGGCCACTCAAAGGCTCTTCGGAGGGAAGCTCAGTCTCGGCTTGGCAGAGTCAGCCCTGGTCAACCTCATACGGGGCTCCAAGCTAAGCGTGCAAGGAAGCAGTCCCACTGCTCTTCCGTGTCAG[G]TCAAGACCACAAGGCAGAIGCCCACTGCTGCTCTTCTCTGCTACTTTCT
2c				
stSG1020	75 AG ---			TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAATAAACATAATCTCCCTTAAGATCCCACCTTATTTTTA[W]GJCTCCAAATAAATGTAATTAATCAGCTGCTGAATT
9b				
stSG1020	34 CT ---			TCTTTTCTCTTTTCACTCTCAGTCACCATGATT[C]TAAATAAACTAATCTCCCTTAAGATCCCACCTTTATTTTTAACTCCAAATAAATGTAATTAATCAGCTGCTGAATT
9a				
stSG1021	29 TC ---			TACTAGACATGCAAAATGAGAAGATTACAT[G]CTGAATATTTAAAGAAAGTTATATTTGTTTGACATAAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
8				
stSG1025	108 AC ---			ATAGGTTTCAGGAACAAAATCAATAAATGGAAAAATGAGAAGAAATCTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTCTCTCTCTTCCCTTGATCA[C]A[J]AGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTCTG
2				
EST10915	123 AC ---			CTGTATTAATTAGAAGGCACTATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAAATCTGTACTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A]CJATTTTAA
0				GAAGTTTCTCTCTCTG
EST11023	166 TA ---			TTTTTTGTTAAACCAACCACCTGAAAGTTCCACATGTGAAATAAGATACACAGTGAACAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAAGTATCCTATACACCAGTAAACAGCAGGGCAATTAGTCAATTAACAAAAAATAGTACATGTTAT[A]JGTGTAATAAAATTAATTTACAAAAGGCTTTTCCACTCGTGGATTGATTCCTTTTTTGGAGGAGGGAGTAATCCTGG
1				
EST14096	71 GC ---			GGGATGTATATTACAGATAACACAACCTCACAAATATACCATCAGACATTTGAAAACTAAGGCCATTCTGTGA[G/C]JTATTTTAAACITGGTGTTTGCACATAATGATCTTAAAAAATAATGAATTACCAAAACCAAGATTCTCTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
8				
EST22113	125 CA ---			TGCAAAATTGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGCAGGGATGCTTAAGTCTTCCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[C/A]CCTTCTCAGGGTCTGTTGGAG
6c				
EST22555	60 GA ---			TCAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAACCTGGAGAGAGAAAGACACTCCCTCCCTAGCTTCTACCTGGGCACCCCTCCAAAGATGAGCATTCATCTGGAGACCAAAATAAAAAAGGACAAAAAGACCAGGGCTCAGAG
7				

EST22917 6	74 C T ---	---	GTAAACCTTGCACACGCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC[CTTGACATGGGCCAAAAGACTTCCAGACAAAGCACGGGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCTCAGGCTGCTCTACTCA[GTGTGGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGGAACCTCAAGAGGATTCACAGATCCACAGTGAAGCAGAAATCATGGGGCAAAAGTC[AG]CTATGG GGCCAGACTGAGGTTGGACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCGCG ACAGCAGGGAGTAGGCAT
EST36745 3	56 A G ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCACCTTAAAAAAACAAAAA AACCTTGCATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTATGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGTATG T[AT]TATGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCACCTTAAAAAAACAAAAA AACCTTGCATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTATG[GT]TTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATAATCCTCACCTTAAAAAAACAAAAA AACCTTGCATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA GGAATTTATGGTTTGAATAAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410a	48 C T ---	---	TATCGTGGGAAGTCCAACTCATACTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC[CT]TTAAATTTGTCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCCCTGAA CAATCTGAAGAGATGCATAGCGGATTTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCCCTCCCGGGATGGTGAATAATGTTCCGGACCTAGATA[CTG]TGACGA AGGTAGCAGCAGACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	GAAATAAACTAAACTGCAAGCAAACTACTGTTAATAAGAAATTGTTCTTCTGTTT[CTGACAGTTG AAGTGGGTGTGAGATGGGATAGCAATGAACAGTGGGAGCCAAATGAGGCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
siSG1026 6	55 T C ---	---	GTATAATTCAGCATAAGCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAATCTTTTACA AGA[TT]G[AAGCAGCAGTAGTACAATAATTTAAGCATCTCAAGTCTCCAATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---	---	CACITTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTTCATACCACGTTGAAACCATGTGTTTATATGCAATAAACAGCAATAATTTTTCACCTC[AT]TG TCAATGCCAATGCATTGAAGGCCCCAGAAATGAGAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
siSG1031 0	128 C A ---	---	

stSG1033	116 T C ---		TTTAAAGCTACATGCTGAAGAAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTCGGGCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATTC/GCATTTCCTCTTTGGCTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTTCCACCTGTTTCATCTGA
1b			CITAGGACCCCTCC
stSG1033	107 A T ---		TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTCGGGCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCAATTCACCTCCATGCATTCCTCTTTGGCTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTTCCACCTGTTTCATCTGA
1a			CITAGGACCCCTCC
stSG1243	225 GA ---		ATTGGCAAAATGGGAAATGACACCAATCAATTTGATTACAGAAAATGGTTTTATAAATCCCTCCTCTTGAAATTTATGTTCCAGCATGGTAGCTTATGCCATCCACGACATTCGGGAGGCCAAGGAGAAGGATCGCTTGAGCCAGGAGTTCACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTTTTAAAAAAAAGAAATCTGTTTC/GA/AAAGTATTTTCAGACCAAAAGGAGGT
b			AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAAATTTGAACCTAGTTTGCTTCTTAC/GA/CGCTTCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1345	60 GA ---		AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAAATTTGAACCTAGTTTGCTTCTTAC/GA/CGCTTCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
b			TTAATGTCATCCAGGAGGGGCCAGGGATGGAGGGGAGGGTTGAGGAGCGAGAGCGAGTATTTTGGGTGGGATTCACACATTTTCCCATGAAGAGGGGAGACTTGGTATTTTG/TG/TCAATCAATTAAGAAACAAAGGGTTTGTAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCOACGACGTTTCAGTCCCTTCTGTCG
stSG1385	117 T G ---		TCGCTCCTTTCCAGTCTCTGCCAGAAGCATCCCATGATGTTGACCGCACAGCACATTTGTGTCCTT/C/GCTTGAGCATTGCCACTCTGGCTGGTCTGCTGCCACTGATTGTACTGCTGCTGCTGCCGATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCATCCCTTGCTCTCCACTCCAGTTTGCTCTGCTCCTCA/T/CJAGTCTCTCTCCATGTGGCAACAAAGATGGCTACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAATCCAGCAGCAAGAAGATGTCTCACTCCCAAGTCCATAACTCAATCCCTTGGGAAG
b			CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGTCCJAG/CTCCCTTGCAATGAATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTTACC
stSG139	69 T C ---		GCA
			CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGT/CJTTTAAATTCAAAGGTTGAGAATGACGAATTCAGAAATTTCTTCATACATAAATGCTTTCCTTAGTCTGCAGATGGGTA
stSG1427	103 T C ---		CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA/C/GJAATGTGGAGGATGCTGTTGCAGCTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAGAGGAAATGCCTGA
b			---
stSG1471	50 A G ---		---
stSG1483	44 T C ---		---
stSG1696	67 C G ---		---

siSG1847			95 GA ---		TTGCAGACAAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTACCCCTAAATGAAAGAATTT AGAGGGTTAAATAAAACAAGTGAGAGACCG[G]ATTTACTTACATCATGTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTTGTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAACACAACTG
b					TTGCAGACAAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCG[G]A/CTAAANTGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCATGTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTTGTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAACACAACTG
siSG1847	a		49 CA ---		CTTAATGCCCTTCTCTCTCTCTGACAGGAGACAGATGGGTAAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[G]GCCCCACCCTCTCTCTCCGGTCTCCCAAGATGACT
siSG1897	a		83 AG ---		TGCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[G]ATTCATTAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGTG TGTTATTTTTCTCCTACAATATTTCTGACTCTGTAGGACAGTGGCCCTCAGTTGGGGGGTTGAC T
siSG2022	a		86 TC ---		AAACGTTGCCAAAAATTGTTTCAGTTTCAACAAGTATAAAAATAAGACTTCTGAAAAAAAAGTTTACA ATTAGTTATAAAACACTTAAAGAATATATTTTGACATT[G]ACATCACAGTGGGGCATTTT
siSG2076			104 CG ---		TTGAGCAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGATTGAGGGGCTCCACAGAGA GAG[G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGCTGA
siSG2108	c		71 AG ---		TTGAGCAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGATT[G]GAGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGCTGA
siSG2108	a		49 TC ---		TTATCCAGGGGACAGCTGCACAAAGGAATGTTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTAATAATCTCAGATGGCAGCACCCTGGCATGGCGAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G]AAGTTCCTATTATATTTAAGGC AGTTTTCAGAGCACTGGCATCTGTTTGGTCTG
siSG2141	b		173 AG ---		TTATCCAGGGGACAGCTGCACAAAGGAATGTTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTAATAATCTCAGATGGCAGCACCCTGGCATGGCGAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G]AAGTTCCTATTATATTTAAGGC AGTTTTCAGAGCACTGGCATCTGTTTGGTCTG
siSG2141	a		113 CT ---		TTATCCAGGGGACAGCTGCACAAAGGAATGTTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTAATAATCTCAGATGGCAGCACCCTGGCATGGCGAGTGGGT GGTGCAAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTTCCTATTATATTTAAGGC AGTTTTCAGAGCACTGGCATCTGTTTGGTCTG

siSG2148	50 A G ---	---	TGGAAACAACCGGCTATAGTCTAGTGCATATTTTAGACCGTGATTTTC[G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGATTTTCGATACCTTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAMCGGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C]TGCCGCGTGACTCAGCTAATGCTACCGGGTTGAGCGCACACCGAGCCCGCCACCTTTTCCAT ACCTGGGCAGAGGGAGGTGAAGGAACA
siSG2189	41 C T ---	---	CAAGTGGTAAAGCTGGGATTTGAGCCGTGATATTCACACTA[C]TCTACATTCCTCCAGTATAATA GGAACCTCATCGTAACTTTGAGCACCTAGTGTCTGAGTACTTCTGATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
siSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGCTGTTCTGTATGATG[C]TTTATATTATGTAT AATGCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
siSG2243	85 G T ---	---	CATTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G]TAGAGCATCTCCTCAGCCCTGGAGACAGTGTGGAGCTTCAGCT
siSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A] C]CTGTCAGGAACTCTGCCAAGCACTGGCTGCTCCTCAGCAGAATTTCTCCT
siSG2306	67 A G ---	---	GTCAACGCGTAGAGGTCACCTGGTATAAACAAACAGTAGCTATATGATAATTTGGGAATAATTTTACA [A]GTATGCTCCCATTTGGGTTTTCCAAACTGATACACCATGAGGTGAACACATTTTCACTGTTTCACAG TTCCTCCAGAGA
siSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT[G]TGCACTGGAGGGGCTGTGGGAGGGTGAATG
siSG2339	63 T C ---	---	AGAGCAGAAATGGTGAATCAACAAGACCTCAAAATTGCTTGAAGTGCAGAGTAAGTGTGCTAC[T]C GTTCTCAGAGTCACCATTAACGGTGACTGTGCTATTCTGGCTGTGCTTCTCTATTCATCA
siSG2465	76 C T ---	---	CAAGCTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCACCTCAAAATG CAGAAACCA[C]TTTACAGATTAAAGAGAAACACACACACACATTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGGGGTATGCA
siSG2549	140 T C ---	---	TTGCAGGCTTGATTTCCACAATAACAAGTCATGTATAGAGAATGTGAATGATACTTGAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTAGTACTGGGTAAATATGCAAGCAGCTAAAG GAATATT[C]TACACCACCCACCCCTTTTAACT
siSG2577	123 T G ---	---	AATTGCCAAATGGAATTTCCAGAGGATTTTAGACCACTTTGCCCTGTGCTATCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAGAGATCAATGCCGAACCGAAGTGTGAAGCAT[G]GAACAATC CCGGCCCAAGATTAAITAT
b			

siSG2577 a	121	CT ---	---	---	AATTGCCAAATGAAATCCAGAGGATTTTAGACCAACTTGGCCCTGTGCAATTCGCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAGAGATCAATGCCGAACCGAAGTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAATATT
siSG2700	58	GA ---	---	---	ATCTCTGAGCTGTTTAGTGGGAAAGGAATCAATTTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTGGGGAATAAACCACTGGTCCAGAGCAGAGGAGCTACTTTGAGCCGGACACCA
siSG2724 b	101	TG ---	---	---	AAACAAGCTTTGTCAATTTCCACTACATTTGTTGTGCTTTATATTAATTTGCAAAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCAAT[G/TT]TTTTTAATCCTGGGGTGTGAAGAAC
siSG2776 a	65	GA ---	---	---	GTGGCCGATCTTTACTTTCCAGAAAGGGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCACAAAA ATATCCACTAATCCGAATATAGTAACCCCTGCTGTCCGAATG
siSG2791 b	109	GT ---	---	---	AAGGAAAGGTGGAGGGAAGAGGGAAGATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2791 a	100	AG ---	---	---	AAGGAAAGGTGGAGGGAAGAGGGAAGATTACAATGGTTAGAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTA/G]TAAATATTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2826	85	CT ---	---	---	CCGCAATTTCAACACACATTTCTATGAAACTAAGGTGGATCATGTACAAACACAAAAAACAAAGC TCCCTCCCTCCAAAAACAAA[C/T]GAACAAAAATAAGAAAGAAACCCATGNAATGCCCAGGTTTA ATTTTTTTCC
siSG2850	88	GA ---	---	---	ATGGGTGCATTGTAAGGCAATTAATACTTTTTCAGGCAGGGCTGGCAAAATTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
siSG3031	71	TC ---	---	---	ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTCTGGCATTCTCTGGTGTGAGC AAAT[C/G]GCCCTTTATTTTAATGATCCAGACATCTGGGCAGCATAGCT
siSG3058	81	GA ---	---	---	GTCCCAACTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAAGAGCATCAAAAGCCAAAAAGGCAAACTGGCTGAGGC
siSG3092	94	TG ---	---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTCTGTCACTATTGAAAAACAAAGCCAAAGTTC CAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTTCTTTATGGTTCCAGCCCCCTACTTT AGTT
siSG3230	95	AG ---	---	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGTC[AG]GTGGGTGCTAAGTGTCTGAAGTGAAGTAG
siSG3245	160	GC ---	---	---	ACATCTATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACACCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGTT[G/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT

sISG3285	42 T C ---			AGGTGAATGAGTACTAATGTAGCATTTATTTATAAGGAATGCGCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTCAGCCACATTCAGTGATGTTTCTAAATACACAAATCGAC AGGACTGTCTGTTCAAGTACAAATGAGGACAGCTTTTCAGGGCAATGGATTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAAA
sISG3289 b	141 C T ---			TGTAATCTGTGTGTCATCCATCCCTCCCTGAGCTGGACTGCTCTCCAAAGGAGACTAGG AGTGAAGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGAC/TTGTAGATCCCAAGTCCCTGACACATTTCTTAAGAAACT
sISG3289 a	24 A G ---			TGTAATCTGTGTGTCATCCATCCCTCCCTGAGCTGGACTGCTCTCCAAAGGAGACT AGGAGTGAAGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTAAGAAACT
sISG3284	130 C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATTTAAATGACTAAATTACAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCCA/C/T TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTTTGTATACCCC
sISG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAAATATACAAATCAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTTAGCTCTCACT/C/ACCAGTGTATCCATTTTCCCGAGCCGTAGAGCTTTCTG TTTCTGTAGATTGCCTGCTCGGACATTTGATATAAATGGAGTGTCTGATCATGTTCCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGATGCGTCAGTCTTCTTCTTAA
sISG3323	26 C A ---			GATCCCGAGTATTATTTCTAAATGAACTTGTGTTGGAAATAAAAATCTGAGGACCACCTCAGAG GG/C/TATAAGGGGAACCCCTTTTGTCTTGTAGTTCATAAGGACTTTCT
sISG3369	69 C T ---			CAAGACTGAAGAACGTAGGCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTCCCAGGACTCAGG CTTCAGCTTCAAAATCCCGAGGAAAGGAATGACATTTCCAACTGTCACTTTGTAGC/G/TCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
sISG3398	125 G T ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAGC/G/GTCTACTGTAGCTGGACCTCC TGGGTTCAAGTGATCTTCCACCTCAGCCAACTGAGTAGCTGGCTGCGAGGACAAAGTCACCATGCTTA CCTAAGTTTTGTAGAGACAG
sISG3416 a	43 A G ---			GTAAGACAAAGTTTGTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCTCCCAAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCCGACCTTTTAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGTAAACACTGAT/AJCAAGTTGCTTAACCTTTGTGAAACCCAC TTTCTTATCTGTAAACAAATGGACAACAGAACTTTTCTTCTCTCTC
sISG3424	173 T A ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCCCT/AJGAAATAGCTTACTCTGTTTCTCCTATC
sISG3436	88 T A ---			

siSG3463	103	CT ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAAATAATACAAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTGCAC[C/T]GGAAACAAACTTGCTTGACTATATTA CTGA
siSG3491 b	71	GA ---	---	CAAGATACTTCATTGTCCTAAGTAGTGCAGTGTGGCAAAATATTTCTCAGCAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTATATACTATTTTCTGTGATG ACAGAAAATAAGTTAAC
siSG3523	33	CT ---	---	TAGCCATCTACTCTAGTTCCTTTTGGGTTTTC/TGTCATATATGTGTGTAACAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCTACCTACACAGCTGCTACAAAAACCAAAATACAGAAATGGCTTC TGTGATACTGGCTTGTGAAACGCATCTCACTGTCATTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTAG[G/T]CCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
siSG3583	112	GA ---	---	GAAGAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586 a	60	GC ---	---	CCTAGTAACATAGTGAGACCTGCTCTACTTAACTCTTTAAAAATTTAAAAATCAGGTGTGGTGG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101	TC ---	---	ATATAGTGTGGTAGCATTTAACTCCTTTAAAAAGCAATCTGGCCATATCAAGGGCAAAAAAAGT GTATATACCACTGTCACAAAAACCCCAATGAT[C/C]CTATTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAACAAAAAGCTATATACAC
siSG3590 a	70	AT ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTTAAAAAAA AA[A/T]TTCTCTGATGTCCTTGACCTGTAGGAACACATTCAGTTTCTACACT
siSG3619	78	AC ---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTGACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40	TC ---	---	ACATATGTAACCTGCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GGATTGAGAGCATGAACCAAGG ATGCGTAATAATCATTTATGAATAATAAGTTATCTGGGGAACCGCCATTTGTCCAACATTTACTAA GTGCTACTA
siSG3646 c	70	GA ---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATATTAACCTTGATACTTGGTTAAGATGGTGTGCTGCTAAATTTCTCCATTTGAGAGTCATT CTTCTCTTTGTA

stSG3646	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATAATATGATGATAACAATA[A/G]TATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATAATATG[A/T]TGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGGAAAAAGG
stSG3693	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGCTCC[C/T]TCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGGAAAAAGG
stSG3698	145 G A ---	---	TCTTGCCCTTTGTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCTTCCTCCTACTGCAGA
stSG3698	51 C G ---	---	TCTTGCCCTTTGTACCCCTAGAGAGATGGCAACCAATCCCAAGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAATAACCCACCTTCCTCCTACTGCAGA
stSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGTTCTCCTGCTGGATCCCAACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATTACCAGCCACAGCAAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTATT[A/J]AAAGTTCCTAAGA CACTGAGGGCATAAACCAAAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGATCTTCCCCCT
stSG3880	115 G C ---	---	GACAAGAGGGGAAGAGATGGCCAGAGACCAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGCGC CACCACACGTCTGTGGTCAAGGCCCTCCTCTCTGGGAGCAGGCTA[G/C]GCGCAGGAGGATGCGAG GGCTGGGAGGGACCCCACTCGGGGACCCAAAGGAGTCCATTCTGCCCC

siSG3880 a	36	G C ---	---	---	GACAAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG[C]GGCAGCTGGGGGTCCCTGAGTGCCAGG CGCCACCACACGCTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGGAGGGACCCCACTCGGGGACCCAAAGAGTCCATTCTCGCCCT
siSG3895	44	A G ---	---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[A/G]TTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAT
siSG3902	104	T C ---	---	---	TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCCGACTCTGGTGGGAACCTTCCTTCGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTCT[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTGTGGACAAT
siSG3935	50	G A ---	---	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
siSG40	25	A G ---	---	---	GAGGAAGAGGTTGAAGAAGTGTG[A/G]AAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGAAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCAA
siSG4009	32	A G ---	---	---	GTGTGGCTGTCTGATGATGAATGGCGGCTC[AGT]ACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
siSG4033	123	T C ---	---	---	AGAAACCTTGGGACAATGGCAGTGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCCTAATGTTTTCAAGCATAAAGGTACTTTT[C]JTGTAAC AGGTGGGCAACAC
siSG4038 a	29	G A ---	---	---	GCTGAGACACGTGTACAGCCACGCCCTGT[G/A]JCGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGACCTGAGGGTTCCATCACT
siSG406	53	T C ---	---	---	ACTGTGGTTCAACAGTATTGCGTTGTGAGACTAGGAAAGCTAAACGAACAAAAT[C]JGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTAAATGGACAGCTTCTTCAACAAGAGATTATTAACTTTTATCAGGTGT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T ---	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGATGATGCTGCTAGATGTTAGTGTATGATGTTATGATGTTATGATGTT GTTTGTCTGTAACTATTTAAAGCTTGTCTTATCTCATCTGTAAACCTATGTGCTTGTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCTGG
siSG4095 a	27	A C ---	---	---	ATCTGGGCTGAATTAGTCAAGCAGGT[C/A]GATACTATTGTCTGCTAGATGTTATGAGGATAAAAA GTTTGTCTGTAACTATTTAAAGCTTGTCTTATCTCATCTGTAAACCTATGTGCTTGTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCTGG
siSG4120	65	G A ---	---	---	TGCATGTTCCACATCTTTTCAACAAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCTCAGAGAGCCCAAGTTAAACAGTTCAGGACACACCATTAATCCACCCAGCT

siSG4128	54 A G ---				CTTGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGGTACATTCTC[AG]TATATTAATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGGG
siSG4209 b	128 G A ---				CACGAAACAGATGCAGCCTACACAGTGTGTAGGACGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCACTCCCTC[G/A]GC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---				CACGAAACAGATGCAGCCTACACAGTGTGTAGGACGAGGCTCACAACATCCACATGGCACAAG /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCACTCCCTCGGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---				CATTACCCAGAACGCCATGGAGGACAGAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGCTGCCTCTCCCGAGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
siSG4301	81 T G ---				TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTGTAGTGGCTCCACACTTTCCAT TTAAGCAATAAATTTG/AGCTTCTGAGTAGTGTGCCAGTTTACCCACATTTTG
siSG4331 b	71 T G ---				CTCACAAGGGCCAAACACAGAAAAGATACAAATACATTCATCCAGCTAATATTAGTTTTATGACAC AGAGTT/GTTTTCAAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCATT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATCTCTTGTGAGGGGTGTC
siSG4340	76 G A ---				TTTTGCAACAACATGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---				TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAAATGTCATCTTTTGC/[A/C]CCTTCAACAATAAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4361 a	24 T C ---				TTCCCAACCATTTGAGTGACAGAGC/[C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAAATGTCATCTTTGCACCTTCACAACACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4376	73 A G ---				TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGCTTCTCAAGGGGAG AACAG/[A/G]CTGGAACGTGGGCTCTGCAAGAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
siSG4381	50 T C ---				GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTT/[C]TCAGTCTTGTAGT ATCCACAGTAGTGCTGTCTGCCATGTACAAGTGTCTGCCAGACACCCCAATTAATTCATGCC
siSG4410	79 A/G ---				ACCAATGGTTCTGCTATGTGCATCCGATAATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACACCGC/[A/G]TGACAACGAACCCAGTGGACTGTGAACACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

siSG443	65	C T	---			AGCAGATCAGTCAGCCACTTGTCTCTCTCTCTTTAGGAGAGGCTAGGCAGTGAACACATCA/C/
siSG4430	54	A G	---			TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGGAGGGAATAGGCAC
a						AAATGGAATCTATCTGCTGTCTCTCTCAGGTC
siSG4448	99	G A	---			ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGT[AG]ATTAAACATA
						GGTAGGATCCAGTTCTCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
siSG4449	92	T C	---			CTCCCTCCCTCTCTCTCTCCCTCCAGTCTTTCCATCTGTTCCCTCCCTCCCTCCCTCCCTCCCTCT
						CGCTAGCCCTGCCCTCTGGGTCAGTGC[G]ATGGGTTAGGCCCCCAAAAA
						ATTAGCCATTCTCTGCAACAATTGCTTTACTGTAACCTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACCTTGGACAACCTTAAACTTAT/CJTAGTGACATTGCTGTCTAATAATCAAAATACITTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
siSG4467	42	C A	---			CAGACATGAGGGATGGCCTGTCTCTCTGGGACAGAGCCTCA/C]A]GATGATGTCCATGTTTGTGT
						GAATGAAACTCAACACTCTTCAGTTTTTAGAGTCAITTTTCTGGTATCGAGCGACACACCGAGGAG
siSG4475	21	A C	---			CACACCTGCTTCCAAGGCTGCTGCCCTTCTGCACACAGT
						ACATGTCATTTCTTGACACAGG[A/C]ATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACACTGGACTTTTGTCTCTTCTTCTTCTAGTACCCAGGTTTCATG
						GTAACATTCTGGGGTGGGGTGAGACAACAC/A]G]ATGAACCAATAATTAACTAATATACATT
siSG4477	32	A G	---			TCAAGGAGACTTTTAACTAGTTAATGTGAACCGCAGCCATCAATGGTTTGTGAGGAAAGGGAGA
						TGAAGTCTTCTGCTGGGGCAAGCTTTGGCCTCATTTGCAGTCAGACTGGC
						TGAACTCAGAGCTGGTGGGAGCTGCAGGAGGGGAGGCTGGGGCCAGATGAGCCGCCGGGGA
siSG4531	79	C T	---			CAGCAGGCGTGC/G]GCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
siSG4550	86	G A	---			GAITCTCATTTGACAGGGGAGACGCTGTGTGTCATCAA
b						TGCATTAAAGGAATGATACGGCATAATTTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATT
siSG4550	85	C G	---			AAAAGACAGTGGGCAC[C/G]CAATTGGAGGGGAAGGGCGGCGAGGTTTATAGAGAAC
a						TGCATTAAAGGAATGATACGGCATAATTTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATT
						AAAAGAGACAGTGGGCAC[C/G]CAATTGGAGGGGAAGGGCGGCGAGGTTTATAGAGAAC
siSG4590	47	A G	---			AATCAGGCACAAGCTCGGGAGAGAAGCCAAACAAAGCTCTTCTGCAC[A/G]ATGGGAGGGAGACAC
						CATTGAAAAGGCATGTTCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCTGGTCTCTCTTG
						AATCTGTATCACCCAGCGTGGT[C]CAATGTACTAGTAGCTTCCACAGGATTTTATACTATTTC
siSG4623	22	T C	---			CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTTTTTCAGCCATTGCAGATTTCACATTTATCT
						TAATATTCTCTTCAAGATGCTCTGGAG
						TAAAAAAAACAACCCCCCAAAAAACACCAGAGTTTTTGTAGTTTTTATGTTTTCAGATTTAAAG
siSG4843	102	A C	---			GTAATTTCTTTCTAGCTTCTAAATTTTGTAGTCA[T/C]ATCAGAAAGTCTTCCCTACTCCCAAGGTGA
						GAAAGGA

[illegible]

siSG6362	88 G C ---	---	---	TGTGAAATGTACACTCAGGCTAACAATAACCTATTATTCTCTGGTTAAGAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAGAAAGGGAAGGAGGAGGAGGAGGACAGATCTGCACAGA AT
siSG8010	62 G T ---	---	---	CACATCTGTGTTCTGGAGCAAGGGAAACACAGAAAGGCCAGGAGTTGGGTGTGCACCTGG[G/T] GTCTTTCAACTGGGTGGAAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAGAAGATAGA TGCCCT
siSG8022	53 G A ---	---	---	AGTCCTGACTCCCTGTTCACTGACGTCATGTTGGTAGCCTGAAATGGACAC[G/A]GTGGGAGTTAT TTACACCATGGAACCTGAAACCTCTACAAATCAATGCGTTATTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGATCTCC
siSG8032	67 G C ---	---	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTACAAATTACTCCAAAGAAATTCAGAAAAATTTGTGT G/C]TGGGAGGCAAGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGTTGGTAAAA
siSG8064 b	46 C A ---	---	---	AGCTGGCTCTTCTCTCTGTCGTGTTCCGGGAGGCTTCACGTCCTCG[C/A]CGTGGTCCCTGGTGGCC TGACGACACAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACAGAGGAACA
siSG8064 a	23 G C ---	---	---	AGCTGGCTCTTCTCTCTGTCGTG/C]TCGGGAGGCTTCACGTCCTCGCCGCTGCTGGTGGTGGCC TGCAGGACACAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACAGAGGAACA
siSG8072	59 A G ---	---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGTGGTCTTGTCTTAGGG[G/V]TGGC AGAGGCAGAAAGGAAGTCGAGTATTAGTGCCCGCATGCAAGTTCAGGCTGTCGTTCAAAA
siSG8100	40 A G ---	---	---	ATACCCACACACCCCCACTCAACCTTGATCAAAATCC[A/G]AAGTGTAACATAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
siSG8102	138 T C ---	---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCCATTAACTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAAACCTTGCATATATTTGAGATGTACAGTGTGATGATACATGTATACAAATGTGAAA TGA[T/C]TGTCAATAATCAATAATCAATATGGTATATTGGTTTAGGAAATGTGATGGT
siSG8105	110 A G ---	---	---	CAGTGGTTCTCAACTCCAGCGTACACGAGGATGGTCTGTGCTTGTAAATACACAGATGACTAGGCC CACCTCGGAGTTCCTGTTGGAGTCTAGGCCCTGAGAAATAT[C/G]TTTCTAACAAAGTCCCAGGTGA CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
siSG8130 b	96 T C ---	---	---	GTGTGATACATATTGGGAATGGAGGAAATAAATGACTGGATGGTCGCTTTTAAGTTTCAAAAT GACATTCCAGACAAGCGGTGCTGAGCC[T/C]GTGCCCTGTCTTTCAGATCTTCACAGCAGAGTTCC
siSG8130 a	36 C G ---	---	---	GTGTGATACATATTGGGAATGGAGGAAATAAATGA[C/G]TGGATGGTGGCTGCTTTTAAGTTTCA AATTGACATTCAGACAAGCGGTGCTGAGCCCTGTGCTGTCTTCAGATCTTCACAGCAGAGTTCC
siSG8145 b	124 T T A ---	---	---	TTGTGGACTTCAAAATCTTCTCCAGATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTTGTGAACACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAAACACTTATCTTAAACTGACTCTCTGCAATCTCTCTGCTGTGAAGG

[illegible]

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCCTCTCTGTAAAGGGAAGTTTGTTCTTGATCTCCATGGGCCAGCCAGCACGTG GTGCCCTGTGAGTCTGTATCAGGTAGGAGATGGACCCAGTGAGGAATTTGAAAGGGCATTG GAAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	---	---	---	GGCTGCCAGGGGTTCCGTGGAGGGGCCCTAGCCGGGGCCCTGCTGGGCTGGGGTCTGGCCACG GTGGAGGCAACCTGCTGGTCATGTGGCCATCGCCCGGACTCCAGACTCCAGACCATGACCAACGT GTTGTAATCTGCTGGCGCAGCGGACCTGGTATGGACTCTCTGGTGGTGGCCGCGCGGCGCCACTT GGGC
ESTD- BA511	--	--	---	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGAGGCTGAAGTGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAAGATGTGCACATGCA
ESTD- BC12	--	--	---	---	---	AGCTGGATTAACTCCTCTCTCTCTGGGGCCGTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGCAGCTGGGAGAACAGGGTACGACAAACCGGAG ATAGTATGAAGTACATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGCCCCGGGGGGCGCCCCGCAACCGGCACTCTCTCTCTCCCA
ESTD-BCR	--	--	---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCTCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTTGCCCGGAAAGGAGGCGAGGTGACAAAGCTAACTCTGCTTCAA ATCAACCATCCGGTGGACACTGTGTGGCTGCACATCTGCTGGCACA
ESTD- BRCA1a	--	--	---	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTTGAAGTTAGCACTCTAGGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	---	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTTCAATGTACCTGAAAGAGAA ATGGGAAATGAGAACATTTCCAACTACAGTACGACAAATAGCCGTAATAACATTAGAGAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	---	---	---	ATGCATCTCAGTTGTTCTGAGACACTGATGACTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTCGTGAAATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGA AATTAGATCCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAAATTTGCTCCGGGAAGCACATTCACAA CCCAGTCAGTTTGGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTTCAACCATGCAATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	---	---	---	

ESTD-C7	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG
	--	--	---	---	---	GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC
ESTD-CB23	--	--	---	---	---	AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAG
	--	--	---	---	---	TAAATAATTGTCTTCATTATGGTCTTTCCGGCCTTCTCTCACACAC
ESTD-CB24	--	--	---	---	---	TAGAACCATCAVAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC
	--	--	---	---	---	TTCAATTATGGTCTTTCCGGCCTTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT
ESTD-CB25	--	--	---	---	---	CTCAGAGCAACCTAGCCCATACCTCTCCCTTCCAGAGGACCTGAAAAACGTGTCCCAOCCGA
	--	--	---	---	---	GGTCGCTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB26	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTTCCTTCCAGAGGACCTGAA
	--	--	---	---	---	AAACGTGTCCACCCGAGGTGGTGTGGAGCATCAGAAGCAGAGATCTCCACACCCAAAAAG
ESTD-CB27	--	--	---	---	---	GCCACACTGTATGCCTGGCCACAGGCTCTACCCCGACACGTGGAGCTGAGCTGGGTGAATGG
	--	--	---	---	---	GAAAGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB28	--	--	---	---	---	GTTTTCTTCAGACTGTGGCTTACCTCCGGTAAGTAGTCTCTCTTTCTCTCTATCTTCGCCGTC
	--	--	---	---	---	TCTGCTCTCGAACCCAGGGCATGGAAATCCAGGGACACAGGGCGGTGAGGAGCCAGAGCCACCTG
ESTD-CB29	--	--	---	---	---	TGCACAGGTACCTACATGCTCTGTTCTTGTCACACAGAGTCTTACAGCAAGGGTCTGCTGCTGCCACC
	--	--	---	---	---	ATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB30	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT
	--	--	---	---	---	TGTTGTTGGGCTGGTTGCAATTCAGGAGTGTCTGTGGAGTCTGCTCATCAGCTATCTCTCTGA
ESTD-CB31	--	--	---	---	---	TTTAGGGAAGCAGCATTCCTTGGAGATCTGAAGTGACAGCCCTTCTCTCCACCCCAATGCTGCT
	--	--	---	---	---	TTCTCTGTTTCATCTGATGGAAGTCTCAAACACCAATTTCCATACC
ESTD-CB32	--	--	---	---	---	AGAATGTATATAGTCTCAAAGTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA
	--	--	---	---	---	GTGGTGACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTTCAGGGTGTCAAGGTGGAAGGT
ESTD-CB33	--	--	---	---	---	GAAAGGGTCCCGTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCTCTTTG
	--	--	---	---	---	GTCAGCCTATTGAGCTGTAATCACCATACCGTIACCT
ESTD-CB34	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAGTTAAGTGACCTATCTAGGGC
	--	--	---	---	---	AATAGACTGAGTTTCTGGGACCTGGAACACTGGACTCTTCTACTGCAGCAGACAAGACTTACCC
ESTD-CB35	--	--	---	---	---	AAGAGAGATTAAATGGCAAAGATATACAAATACAAATTTTATTTGACCAAAACACTATCATGGAACAGC
	--	--	---	---	---	ATT
ESTD-CB36	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCAAATGTGGAGAGGGCCTTAGAAGACATGTTTGATGCCTTAGAA
	--	--	---	---	---	GGCAATCCATCAAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCTCATCATGAAAC
ESTD-CB37	--	--	---	---	---	TGGGAGGCGGGCATAGTCTCATGCCCTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC
	--	--	---	---	---	TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACAT

[illegible]

ESTD-D7S399	--	--	--	--	--	TGAATCTTAATTGCTATCTCTACAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTCTTACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	--	GTGGGGACACGAGGGCTCCAGGCTGGGGCTTGACGTGGCTGAAGCAGCTGCTCGGCTCCACT TCCATGGGTGGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	--	--	--	--	--	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCATCAC ACAAACGGTCAGCACCCCACTGAACCTCGAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD-DRD2	--	--	--	--	--	TCTGCCTTTGGTCAGGAGGCTGCGGGGAGGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCACTGACTCTCCCGGACCCG TCCCACCAAGGCTCCACAGCACTCCGACAGCCCCCGCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	--	--	--	--	--	AAGCAGTGGCCAGGATGAGCGGCGAGTAGGAGGAGGATAGAGGATGGGGGGGCTGGCTGG CACCTGTGAGTCTCTGCCACAGGTGTAGTTCAAGTGGCACTCAGCTGGCTCAGAGATGCCATA GCCCCAGGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD-ERB82	--	--	--	--	--	TCCTTTCAGGATCCGATCTGCGCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACAGCTGG GGTGAGGGGTGGTGGTGAGTGCCTGGGGGGCGGTCCAGACCCACCGGGCTGGGAGGACTTCAACC CGCTCACCTCCGTTCTGTCAGCAGTCTCCGATCGTGTACT
ESTD-ETS2	--	--	--	--	--	ACTCACAGTGCCTTTAAGTGAATGGTCGAGAAAGAGGCAACAGGAAGCCGCTGCGGCTGGCA GTCCGTGGGACGGATGTTCTGGCTGTTGAGATTCTCAAGGAGCGAGCATGTCGTGGACACAC AGACTATTTTAGATTCTTTTGCCTTTTGCAACCAGGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	--	--	--	--	--	GATAAGTACACTGAGGCCCCAGGAGGTATTGCCTAGTAGOCCAACTGTGTCATGCAGGCTTAACCTCT GCACCAATGGCCTCAAGGCCGCTAGGGGAACCTGGGGGATCTAGGGGATGGTGAGGAATGGCC AGCCAGTCCCGGGCGGTGGTCCCAACAGAGGAGGCGCTGGAGGAGGAGACAGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	--	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTAAAGTATGATGTTTAAAGTCAAACTCATTTTTTTTCCATA GGTATGCCAATTTAACCAGCACAAATTTGTTAAACAAAAAAC

ESTD- G0DH	--	--	--	---	---	CGCAGACCGGTGAGTGGGGTCGGAGGTGGAGGGAAGGAGGAGGAACCTGGGGTTTAGGGACT TTCCGGGGTACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGGAGAACACAGAGCACAAGCTGGCTAA GTGTAAGGGACCTCTGTGCGCACCGGTGTCTGCTGCCCTGTCAGCTGTCTGTCTGCCGACGTGGA CTCTGTCCCGGAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTATGTCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGTGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACACACCTGGCTGG AGCAGGAATGCCAGCGCGCTGAGCCCGCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCCTGAGTAOCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAACCACAGGCATCATTTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTCGGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACACATCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAACGCCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAOCTTAATTACACCTGAGCAACAGAGTTCCGGCTCCGGCTTGATCC AGATGGAGCTTCTTTATCCCTGATGATTGGATTGGCTTCTGCTG
ESTD-HT2	--	--	--	---	---	GGGTAAAATTCGAGCAACTTGCATAGACTGTTTATTTGACTTGACAGGATGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTGTGACAGAGAGAATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTAGGTTCTTGGTGCTTCTATCGGCAAGAAATCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTCTGACGAGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCCGGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGTTTACAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGTTTCTCTCTTCTATCTTATAGATTGATGTATGCTCTCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATTTCTCTCTACAAAATGAAA ACATTTCTGCTCTGTAAATCCCTCGAAAGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCGCTCATTTGCACGGTCTTGGCAGGAGTGGCCCTGGGAGAGAAGGAAGATGTTT CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTCAATGGATACAGAAATTGTGGGAGTCACATATATCTCTATGAACAAAAATTCAGATT CAGTGTAAAGTAATGTTCCCTACATTGTGTGAGTGACGGGCGAGTGGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTACAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACATGAAAGT ATGTAAATACTTCCAAAAATACATAAAGCGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	---	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTATTATTTATTTATTTT AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGAGTGGCAATCTCGGCTCACTGCAAGCTCTG CCTCTGGTTTCATGCCATTCTCTGCTCAGCCTCCGAGTAGTGGGAATACAGGCAACCCGCCACT GTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTACCTGGGTGCTCTCTGCTCCTCAGGAGCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGTTTTTAAATAGTCTC TGCCAGATACATCTCCCCATATAAAGTTATAACCCAGTATTGATA
ESTD- KRT8	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCGAGAATGTTAAGTACAAAAAGTGAGGCCCATAG GCTGCCATCTCTCCCGTCTCAGGTTTACCACGTCACCATTTGACACA
ESTD- LF79	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTGAACCGTAGCAAACTGCATTTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTCTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCCAGGAGGGCTCCCTTACCACCCAGA
ESTD- LMP2	--	--	---	---	---	TACACACTTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	---	---	---	TGTCAGTGTCCCTAGGGGCACCTCAACCCTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCTGCA AGGGTTTTGCTTAAATTCAAATTCAAATGCTCTTCATCTTTTAGCAGCTGTGGGGTTTTGTGTGTTTC TTCTGTTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTTCACCTG
ESTD-MCC	--	--	---	---	---	TTGTCAGGAGTGTCTGATGCTGCCTCCCCAGCTCTGTCCCTAGCCGAATTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGTTTGGTCTAAGTTGCTGAATACCCGGAATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCTCTGTTTAGCATGG
ESTD- METH	--	--	---	---	---	
ESTD-NF1	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCCAACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAAAA AAATTTAAAGGGGTACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGAGAGAAAGATCATTTGAAATTTCTGAG AAACCTCTTTTAAACCTCACCTTTTGGGGGTTTGTGAGAAGGTTATCA
ESTD- NPPA	--	--	---	---	TGTCCCTAGGCCAGCCCTGCTTGTCCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCOCACAGAACAGAGAGCGGCCCTCAGTG TATCCCCACCCCAATGTGGGCGCTGGAGATGAAGAGGAGTTGATGCAAGT
ESTD- NRAS	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGTGATATTGGATCTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTC ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	---	---	GTGACCTTCTACITTTAAAAACTTTACGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGTATGTAAACA
ESTD-PAI1	--	--	---	---	GCCACCAACCCACCCAGCACACCTCCAACTCAGCCAGACAAGTTGTTGACACAGAGAGCCCC TCAGGGGCACAGAGAGTCTTGACACGCTGGGAGTCAGCGTGTATCATCGGAGCGGCGGGCAC ATGGAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTAGACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	CTCTTCAGGAACCAACAGTCTTTACCAAAACAGCACTTATGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTAGTGTCTTCTACACTTCTGTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
ESTD- PBDA	--	--	---	---	CCTTCTCATGCCAGATGAAATCCAGTCCCTCAGGATCTGCCAACTGTGACAGTCTAAAGAGT CTGAGCGTGGCTGGGAAGGGCAGGACTAATCCAATCTTACCCGACGTTGCTCGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	---	---	GGGAGTAAACTTGGATTGGGAGATTTCTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTTCGTAGCCATATTAATTGGTTGTGCTTACATT ATTACTCCTTGGCATTTCAGAAAGCATTCCAGCTCTCCCAATCTCCATCACCTTTGGGCTTGT CTACTTGGCACAGATTATCTTGA
ESTD- PXPPI	--	--	---	---	ATGAACATGGTCTTTAATTTTATGATATGTTTGTATTAGCTATCTTAAAGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGTGCTCCCTAGAACATTTTGAAGAGGTAAGTCTTATGAAATTAATCTT
ESTD- Pai/RDS	--	--	---	---	ACCTACAGACGTCGCTGGATGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTGGCGGAGACCTTGGAAAGGCT

ESTD-PDS	--	--	--	---	---	---	CCCGAGGAATCTGAGCGGAGAGCGAGGGCTGGCTGCTGGAGAAAGAGGGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAAGGAGTGAAGCCGAGGCGCGAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAAACACTGAGAAATAGTGCAC CCAGAAACGTGGATCTCCGCTCATCAACTCCGAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTCGTGACGGGAGGTACAGTCTCCGCTCTTTATGGACATATGGATGAGTGTCTGACCATTTCC CTGTGACAGTGTACAGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACATCATGCCCGC TCCCTGTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTACCGGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTCTCTCTGGAGCCCTGAGGAGTGTGTGTGTGTG CAGTCCCGCGCCACCTGTGTGTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACACACCTGGCCATGTCCCTGGCCTGTGTGTGACACCCCTCTGTGAACCCCCAACCCCTGCCCTCC CCCCCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTCACTTTGTGGATTGTCTTTCTGTGTGCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGGCTGTGTGTGGGATATTTGAAGAGATCTTGGCAGTCCCATGTCTCTAGAGAG TTTTCCCAATGTTTCTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTGATTCTGTGA
ESTD-TAT	--	--	--	---	---	---	AAATGTGAGGACCCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTGTGTACACCTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THPB	--	--	--	---	---	---	TGGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCGAAGAGAAAGAGTCCCAAG CACACGAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCAGACAGGATCACTTCATCCA CACTGGATTGGCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGCCCCAACTTCCAAATCCCGCCCCCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTGAGTCTGTGGATTCTTGTTCACCCAGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGTCTTCAATGGGCAAAATCAATGTCTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTTGATGTGCTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AANCTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTGTATTTCTTTCACATTTATTACCTCTCTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCCAAGGCTCAATACAAGCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGATCACCAGAGCCCAAGACACAAGGTACAGACAGACAGGAACACCCAGTG ACTCTGAGATGTCACAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-WVF	--	--	--	---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGMVGGAGAGAATGGACCTACCTTCCACACTGTCTCTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTCCGATCTGAGACCAGTGAGAAACGCCCTT CATGTGTCTTACCCAGGCTGCA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAANA TATCCCAAAGTTGAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACCC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAAACCACCTGACAGATACCAGCTGTTGGTGAAGG AGTGCCCACTCCAGGGTGACACTGGACAAGAGAGGCATCCAAGG
EST52418 6	--	--	--	---	---	CAAAATACAGGTCACCTGCTATGATGTGTTGGAGCCCAGTCACCCITTTGGTGCTACAAGATGCTG GGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTTAAGTTCACATTTGCCAGGA CCAGTGAAGCAACAAGGGCCAGGGCTGGCTTATCAGCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGGAGAAGGAGGTGCGTCTGCTGCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	AGGCAGAACTGGGCCCCCATGCGGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAAGAGGACCTGA GGGACAAAGTCAACTCTTCTTACGACCTTCAAGGAAAGAGAGCCAGGACAAGACTCTCTCTCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGACAGCAGCAGGAGGTGCAGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCCCTGGTGC

EST10398 2	..	--	---	---	---	---	TGCCTGGGTGGCAAGGCTGCAACAAGGAGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTATGATGATGTTACATTTGGGCTTGACCTTCCAAACACGGAGAAG CATTTGTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATAGGCAITTG
EST36751 7	--	--	---	---	---	---	CCAACTCGTTCAATTTTAGCTTTGCAGGTTTTAACTCGATTACTTTTCTTATCAAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	--	---	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAAATAAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAAACAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	--	--	---	---	---	---	GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACITTCGAAGGTAAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	---	TTCCGGCAGCCCCCATCTCTGGCACCCCTGGTCCCTCAGGGGCCAACCCTGGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCGGGCGCGCTCTTGAGACATAGCTGGACCGTTTCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCCAGGGGCCAGCCTGCAGAGAGAGGGTCCCTGTGTGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGCCAAATTCGAGAGACCTAGAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTGGTAGGCCAGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	--	--	---	---	---	---	AGACCATGAAGGAGTTGAAGGCTACAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCAACGGCTGTCAAGGAGCTGACGGCGGAGGGCCCGCTGGCGCGGACATGGAGGA CGTGGCGGGCGCTGTGTCAGTACCGCGGAGGTGCAGGACATGCTGGCCAGACACCGAGGAGC TGCGGGTGGCGCTCGCTCCACCTGGCAAGCTGGTAAGCGGCTCTC
EST43211 8	--	--	---	---	---	---	CGCCTGGTGCAGTACCGCGGCGAGGTGCAGGOCATGCTGGCCAGAGACCGAGAGCTGGGGTGGC CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAAAGCGCC TGCCAGTGTACAGGCGGGCGCGGAGGGCGCGGAGCGGCTCAGCGCCATCCGCGAGGCGCTG GGGCGCTGGTGAACAGGGCGCGTGGCGGCGCGACCTGTGGGCTC
EST36770 4	--	--	---	---	---	---	TGTAGCCAAAGTCACTGCATCATATTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATAATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACGGGTTTCTGTTCTCTTCTGATCAT TCTTACAAGTTATACITCTATTGGAAAGGCCCTAAAGAGGCTTATG

EST26021 1	--	--	---	---	---	TAATGTAGCTCATCCACCAAGAAGCCCTGCACCATGTTTGGAGTTGAGTGACATGTTGGAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACATTCACCTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAAGCAAGCC
EST51212 0	--	--	---	---	---	ATCTGAGCTCGCCAATAAGCTTCTGGTTCTACTTCTCTCTCCACAAGCCCCAAATTCACCTTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	---	---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGGTTAATCTGCTCATGACGCTGGGCTGGGTCOCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGACGGGGTCTCTGGGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGGGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	---	---	---	ACAATCCAGGTCACACATTCAGAAGAGGAGGGGTGGTCACTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	---	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTACAGGTGTTAATAGTGAAAAG GAAGTTGCAGCTCATGACAAATTTGAAGCTGACAATACACAAGAAAGGAAATAAATTCACAGTCAA AGAATCAAGCACATTTTGAACAATGAAGTTGTTTGAAGTGGTGTACACCTTTAATACAAACCTAG CAGACGGAAGTGAAGTCAAGGTAAGAAT
EST34088 2	--	--	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCCAAGAGACCGGCTCAAGG ATCCCAAGGGCCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGAGGACCCAGAAAT CACAGGTGGGCACGTCGGCTACCGCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	---	---	---	TCCAGGTGGCTGGAACCCAGGCCCCAGCTCTGCAGAGGAGGACGTGGCTGGCTGGAAGCATG TGGGGTGAGCCAGGGGGCCCCAAGGAGGGCACTGGCTTCAAGCTGAGCTGAGCTGAGCTGAGCTG CCAGTCACTGCTCTTCTGCCATGGCCCTGTGGATGCGCTCTGCGCTGCTGGGCTGCTGGGCTC TGGGGAAGCTGACCCAGCCGACGCTTTGTGAACCAACAGCTGTGGC
EST45311 0	--	--	---	---	---	GCCCTCCTCTCTCCAAATCTGTCCTCTATAGTTTCTCTATTAGTGAACATACATGCAATCTTTTAGT GGATAGTGCACACAACACACAGGCCATTATGGGGAAGGATCCAGGTGTGGCCCATATTGTAAACA CATTTTCTGCAAAATCACCTCTTTTCATTAAACAGCCCTTATCAATGGCCCTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST65258 8	---	---	---	---	---	TGCCCCATACGGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAAGAAAT CCAGTTATTTTCCAAOCCCTCAAATGACAGCCATGGCCGCGGCTCTCTGGGGGCTCGTGGGGGGG ACAGCTCCACTCTGACTGGCACAGTCTTTGCAATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	---	---	---	---	---	ATCAGAGTGAAGGTGGACAGGGAGGAGGGCCAAOCTGTCTCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 ..	---	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCCTCGAAGTCCAGTATTCACAGAGTTTGGTTTTGAAGTACATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGCTTGGGGTTTTTGGTGATGCA
EST35879 9	---	---	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGTTCCACCGATG GAAGTCCGGGCAATCCTGACAGCTGTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACACAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	---	---	---	---	---	GGAAGAGATTAAAGAGCTTGATTGGACAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACACAGAACTCCTTTAGTACAGCGAGTAATAGATATATTCACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045 6	---	---	---	---	---	GGAATATTAAAAATTTTAAATACCTCCATTTTGTCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTGGCAATTTGTTTCTTACAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	---	---	---	---	---	ATCACAGTCTCTGTCTCTGGCCATCTTCTCTGGGAGAGATGGATGGTGTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590 --	---	---	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136 --	---	---	---	---	---	TGAAGCTTCTGCCCCAGCTTGCATTGTTTCTAGGAGAACCCGGTCTACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	---	---	---	---	---	CTCTGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGAGAACAGGACAGCCACATGGCGGGATGGCCGGGGAGTTCTGGT TGCGGCACAGGCTGTGGCTGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT TGCCCAAGGAGGGGGGGTGGCCATGCCTGAGATGTAGATGGGCGC
						Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

- 305 -

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

- 306 -

CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

-307-

12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

-308-

20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.